## Port, Toby

From:

Swope, Sheridan

Sent:

Monday, July 18, 2005 11:49 AM

To:

Port, Toby

Subject:

FW: 10/674,636

I do not have the results from this search request. Was it completed? Would you send me the results?

----Original Message----

From:

STIC-Biotech/ChemLib

Sent:

Monday, July 18, 2005 11:39 AM

To: Subject: Swope, Sheridan RE: 10/674,636

Call 22523 Toby Port.

----Original Message-----

From:

Swope, Sheridan

Sent:

Monday, July 18, 2005 11:23 AM

To:

STIC-Biotech/ChemLib

Subject:

FW: 10/674,636

Who has this search request?

----Original Message-----

From:

Swope, Sheridan

Sent:

Wednesday, June 15, 2005 3:59 PM

To:

STIC-Biotech/ChemLib

Subject:

10/674,636

For 10/674,636, pls search and interference search:

SID 2 regular full-length against the AA databases

SID 2 oligo search (≥50AAs) against the AA databases

THANKS!!

Sheridan Swope, Ph.D. Patent Examiner, AU 1652 Recombinant Enzymes 571-272-0943 (voice) E02B71 Remsen Bld (Office) E02C70 Remsen Bld (Mailbox)

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## ALIGNMENTS

Carboxylesterase; enzyme; human; analgesic; nootropic; antiinflammatory;

diagnosis; therapy.

Human carboxylesterase family member 53010.

23-SEP-2002 ABB79537;

(first entry)

ABB79537 standard; protein; 581 AA

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RESULT 1
ABB79537
XX Huma
XX Carti
FT Prot
FT Prot
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Peptide
                          53010 nucleic acids, useful for diagnosing and treating e.g. vascular diseases, autoimmune diseases, or neurodegenerative diseases, as surrogate markers, in tissue typing and chromosome mapping.
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28-MAR-2001;
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DB; ABN84302.
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2001US-0279508P.
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RESULT 2
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Best Local Similarity 100.
581; Conservative
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 ADQ89094 standard;
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                                                                                                                   EGATÉÉÉKILÉRKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNWSI
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protein;
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Pred. No. 1e-278;
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04-FEB-2003; 2003US-0444783P

27-MAR-2003; 2003US-0457901P

08-MAY-2003; 2003US-0468775P

19-MAY-2003; 2003US-0471614P

16-UUN-2003; 2003US-0478742P

18-UUL-2003; 2003US-0498529P

30-UUL-2003; 2003US-04991156P

02-SEP-2003; 2003US-0499594P

26-SEP-2003; 2003US-0499594P
                                                                                                                                                                                                                                                                                                                                        Sequence 581
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Pred. No. 1e-278;
Mismatches 0;
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20-DEC-2000;
09-JAN-2001;
30-JAN-2001;
06-FEB-2001;
19-MAR-2001;
04-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wound healing disorders; atherosclerosis; Parkinson's disease; Alzhaimer's disease; autoimmune disorder; haematopoietic disorder; inflammation; neoplastic disease; nervous system disorder; cardiovascular disorders; pancreatitis; respiratory disorder; hyperproliferation; systemic autoimmune disease; hyper-immunity; developmental abnormality; gastrointestinal ulceration; neuropathy haematological disease; metabolic disease; sperm dysfunction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytostatic; vulnerary; antiarteriosclerotic; antiparkinsonian; nootropic; neuroprotective; immunosuppressive; haemostatic; antiinflammatory; cardiant; antiuleer; virucide; antithyroid; cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP61004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thyroid disorder; hypothyroidism; brain damage; colitis; cone photo- transduction deficiency; neurological disease; stroke; angiogenesis; ovulation disorder; spinal cord; thyroid gland; hear trachea; thymus; lymph node; muscular system; obesity; anorexia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-SEP-2002
                                                                                                                                                                           19-DEC-2000;
                                                                                                                                                                                                                                    17-DEC-2001;
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2000US-0257048P.

2001US-0260482P.

2001US-0264922P.

2001US-0266797P.

2001US-0276988P.

2001US-0281535P.
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CC which allow it to be secreted extracellularly or membrane associated. The cativity of polypeptides of the invention may be described as, cytostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic, crediant, antiulcer, virucide, antithyroid, cerebroprotective, immunosuppressive, haemostatic, antiinflammatory, cc cardiant, antiulcer, virucide, antithyroid, cerebroprotective, anorectic, crediant, antiulcer, virucide, antithyroid, cerebroprotective, anorectic, cc and metabolic. Polypeptides and polynucleotides of the invention are cc useful in the treatment, or as a vaccine in the prevention of, cancer, cc wound healing disorders, infection, atherosclerosis, Parkinson's disease and polynucleotides, parkinson's disease and folynucleotides of the invention are cc and Alzheimer's disease, autoimmune disorder, haematopoietic disorder, inflammation, neophastic diseases, nervous system related disorders and cradiovascular disorders, pancreatitis, respiratory disorders and cardiovascular disorders, pancreatitis, respiratory disorder, thyperproliferation, systemic autoimmune disease, hyper-immunity, cc developmental abnormality, sastrointestinal ulceration, neuropathy, cc daisorders e.g. hypothyroidism, brain damages, colitis, cone photoctaristic and diseases, stroke, angiogenesis, coulties, cone disorders, diseases in the spinal cord, thyroid gland, heart, crachea, thymus, lymph node and muscular system, obesity, anorexia, cc growth abnormalities, and alleviation of precocious puberty. The sequences given in records ABP60965-ABP61019 represent novel human cc proteins of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1(a); Page 312-313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parkinson's
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(SMIK )
(GLAX )
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                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          creted proteins and polynucleotides useful as vaccines for preventing treating various diseases e.g. cancer, wounds, atherosclerosis, rkinson's disease, Alzheimer's disease, infection, autoimmune disorde
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Smith RF, Strum
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rum JC, Xie
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                                                                                         HKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQ
                                                                                                                                                                                                                                                                                                                    WCFFLILQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVPLGVPFAAP
LALHLIQNILHIPPQYLHLVANEYFHDKHSLTBIRDSLLDLLGDVFFVVPALITARYHRD
                                                                                                                                                        WDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLF
                                                                                                                                                                                                                                              PIGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHMLKVHYPKFGVSEDCLYLN
                                                                                                                                                                                                                                                              PLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHMLKVHYPKFGVSEDCLYLN 131
                                                                                                                                                                                                                                                                                                  WAIWVLAAP----TKGPSAEGPORNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAP
                                                     KTKS FTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPMKEAPEILSGSNKS
                                                                                                                                           WDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLF
                                                                                                                                                                                                            IYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTT
                                      KTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPMKEAPEILSGSNKS
                                                                                                                                                                                              IYAPAHADIGSKLEVLVWFEGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTT
                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 2.3e-263;
3; Mismatches 6;
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RESULT 4
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AC AAE25025
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                      Sanjanwala MM,
Lee EA, Ding L,
Lal PG, Warren |
                                                                                                                                      08-DEC-2000; 2000US-0254308P.
15-DEC-2000; 2000US-0256189P.
21-DEC-2000; 2000US-0257711P.
19-JAN-2001; 2001US-0267706P.
02-FEB-2001; 2001US-0266020P.
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      Au-Young J, Baughn MR, A:
a AJA, Tang YT, Yue H, T:
g J, Walia NK, Nguyen DB,
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Length 642;

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Sequence 642
                                                                                                                                       The invention relates to an isolated human drug metabolising enzyme (DME) and its nucleotide. DME is useful for diagnosing, treating or preventing disorders associated with aberrant expression of DME, where the disorders
                                                                                                                                                                         Claim 65; Page 155-156; 169pp; English.
                                                                                                                                                                                          Novel human drug metabolizing polypeptide, useful in diagnosis, prevention or treatment of autoimmune/inflammatory, cell proliferative, neurological, developmental, endocrine, metabolic and gastrointestinal
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N-PSDB; AAD40574.
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DLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIPLILSASDMLHSPLSSLTFLS
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                                                                                    VANEYFHDKHSLITEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVVFYEFRHRPQCFED
                                                                                                                   DĹĹSÓKAFKAÍPSIÍGVNNHECGFĽLPMKBAPEVĽSGSNKSĽAĽHĽÍQNÍĽHÍPPQYĽHĽ
                                                                                                                                  DLLSQKAFKAIPSIIGVNNHECGFLLPMKEAPEILSGSNKSLALHLIQNILHIPPQYLHL
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                                                        The invention relates to novel diagnostic and therapeutic polynucleotides CC selected from one of the 2722 sequences defined in the specification. A CC polynucleotide of the invention may have a use in gene therapy. The human CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be CC used to diagnose a particular condition, disease or disorder associated CC with human molecules, e.g. cell proliferative disorder, endocrine CC autoimmune/inflammatory disorders, gastrointestinal disorder, endocrine CC disorder, neurological disorders, gastrointestinal disorder, endocrine CC infections caused by virus, bacteria, fungi or parasite. The dithp CC molecules may also be used in genetic mapping, in identifying individuals CC from minute biological samples, in detecting single nucleotide CC golymorphisms, as molecular weight markers, and for somatic or germline CC gene therapy. The present sequence represents a dithp protein of the CC invention. Note: The sequence represents a dithp protein of the printed specification, but was obtained in electronic format directly CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F; Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV; Mooney EM, Delegenne AM, Panesar IS, Banville SC, Reddy TP; Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH; Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL; Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES; Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzer Patury S, Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
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N-PSDB; ACN42766.
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12-SEP-2002; 2002US-0410260P.
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Query Match Best Local Similarity

94 . 64

Score 2900; DB 8; Pred. No. 7e-262;

Length 642;

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RESULT 6
ABP61005
KW mootropic; neuroprotective; immunosuppressive; haemostatic; watinflammatory; cardiant; antiulcer; virucide; antithyroid; watinflammatory; cardiant; antiulcer; virucide; antithyroid; cerebroprotective; anorectic; metabolic; vaccine; cancer; infection; wound healing disorders; atherosclerosis; Parkinson's disease; wound healing disorders; atherosclerosis; Parkinson's disease; inflammation; neoplastic disease; nervous system disorder; inflammation; neoplastic disease; nervous system disorder; wardiovascular disorders; pancreatitis; respiratory disorder; hyperproliferation; systemic autoimmune disease; hyper-immunity; wateriory dispersonitestinal ulceration; neuropathy; wateriory disorder; hypothyroidism; brain damage; colitis; whipper disease; metabolic disease; sperm dysfunction; whyperproliferation disorder; hypothyroidism; brain damage; colitis; whipper photo- transduction deficiency; neurological disease; stroke; wateriory hypothyroidism; brain damage; colitis; whipper photo- transduction deficiency; neurological disease; stroke; wateriory hypothyroidism; brain damage; colitis; wateriory hypoth
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09-JAN-2001; 2001US-0260482P

30-JAN-2001; 2001US-0264922P

06-FEB-2001; 2001US-0266797P

19-MAR-2001; 2001US-0276988P

04-APR-2001; 2001US-0281535P

08-MAY-2001; 2001US-0289622P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder
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WDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGBSAGAISVSSLILSPWAKGLF
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                                                                                IYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTT
                                                                                                                                                      PLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHMLKVHYPKFGVSEDCLYLN
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SMITHKLINE BEECHAM
GLAXO GROUP LTD.
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A, Rizvi SK,
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  21-MAR-2002;
                                                                                    Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease.
                             19-MAR-2003
                                                    EP1293569-A2
                                                                           Homo sapiens
                                                                                                                                                  Human protein,
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Seki N,
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N-PSDB; ADA53168.
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24-JAN-2002;
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Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
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The present invention relates to novel human secretory or membrian proteins (ADA54072-ADA55710) and their coding sequences (ADA524 ADA54071). The coding sequences are useful in the gene therapy diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.

secretory or membrane J sequences (ADA52433-

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Best Local S
Matches 501
                                                                                                                                                                Human; NOVX; metabolic disorder; cardiomyopathy; diabetes; ASD; hypertension; congenital heart defect; actric stenosis; valve disease; atrial septal defect; atriventricular canal defect; ductus arteriosus; pulmonary stenosis; subacrtic stenosis; ventricular septal defect; VSD; tuberous sclerosis; scleroderma; atherosclerosis; infectious disease; obesity; anorexia; neurodegenerative disorder; Albeimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; haemophilia; hypercoagulation; Crohn's disease; cancer.
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19-JUN-2001;
12-SEP-2001;
25-SEP-2001;
25-SEP-2001;
27-SEP-2001;
17-CTP-2001;
17-CTP-2001;
14-NOV-2001;
14-NOV-2001;
14-NOV-2001;
21-NOV-2001;
04-DEC-2001;
04-DEC-2001;
03-JAN-2002;
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19-APR-2001
20-APR-2001
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23-APR-2001
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2001US-0282930P.
2001US-0282931P.
2001US-0283512P.
2001US-0285381P.
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2001US-0286069P.
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2001US-0391649P.
2001US-0332131P.
2001US-0332131P.
2001US-0332115P.
2001US-0332115P.
2001US-0332115P.
2001US-0345761P.
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2002US-03457621P.
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Guo X, Kekuda R, Miller CE, Malyankar UM, Spytek KA;
Patturajan M, Liu X, Gusev VY, Li L, Vernet CAM, Zerhusen BD
Gorman L, Shenoy SG, Pena CEA, Stithson G, Burges CE, Gerla
Padigaru M, Shimkets RA, Gangolli EA, Taupier RJ, Casman SJ,
Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DJ;
Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman JA; Ellerman ᄌ Spytek KA; et CAM, Zerhusen BD;

2003-046858/04.

New isolated NOVX polypeptide useful for treating atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease and cancer.

Claim 1; Page 303; 666pp; English.

The invention relates to human polypeptides, termed NOVX, and the polypurcleotides encoding them. The polypeptides and polynucleotides are useful for diagnosing disease, and screening for potential therapeutic agents. The sequences are useful for treating metabolic disorders, cardiomyopathy, diabetes, hypertension, congenital heart defects, articles, atrial septal defect (ASD), atrioversit stenosis, entricular canal defect, ductus arteriosus, pulmonary stenosis, subsortic stenosis, scleroderma, septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma, atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease, parkinson's disease, immune disorders, haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease and cancer. Sequences ABUS4542-ABUS4647 represent human NOVX polypeptides haematopoietic disorders, and cancer. Sequences ABU of the invention

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06-OCT-2000;
20-OCT-2000;
09-NOV-2000;
16-NOV-2000;
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Best Local S
Matches 497
                                                                                                                                                                                                                                                                                           drug metabolising enzyme; DME; cytostatic; immunosuppressive; antiinflammatory; endocrine; ophthalmological; gastrointestinal; hepatotropic; cancer; cell proliferative disorder; autoimmune disorder; inflammatory disorder; endocrine disorder; eye disorder; gastrointestinal disorder; liver disorder; metabolic disorder; enzyme;
                                                                                                                            28-SEP-2001;
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2000US-0236947P.
2000US-0238864P.
2000US-0242323P.
2000US-0247581P.
2000US-0249519P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WVQKNTEFFGGDÞŚŚVŤÍFGEŚAGAÍSVŠSLÍLSÞMAKGLFHKAÍMESGVÁIÍÞYLEAHD
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                                                                                                                                                                                                                                                                                                                                                                                                                                      metabolising enzyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REATSYPNICLIONSEWILLIDOHMIKVHYPKFGVSEDCLYLNIYAPAHADTGSKIPVILVWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REATSYPNICLONSEWLLLDOHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVWF
                                                                                                                      2001WO-US030662.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry.
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94.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     618
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Pred. No. 1.2e-233;
4; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                        (DME)-2 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,
6
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밁 Ş 밁 5 밁 S 밁 8 В Ś

451 489

TKPAPYKADHADEVRFVFGGAFLKGDIYMFEGATEEEKLLSRXMKKYWATFARTGNPNGN TKPÁFVKADHÁDEVRÉVFGGAFLKGDI VNFEGATEEBKLLSRKMIKYNÁTFÁRTGNENGN

548 510 488 450 428

vane v prokristie i rosiloli gove povojal i tary projega povoje preprintoga povoje projekti povoje p VANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYBFRHRPQCFED

429

392 391

DLLSOKAFKAIPSIIGVNNHECGFLLPM-

331

DULSQKAFKAIPSIIGVNNHECGFLLPMKEAPEILSGSNKSLALHLIQNILHIPPQYLHL

YBKŚEDLOVVAHĖCONNASOSEALLRCLRTKPSKELLTLSOKTKSFTRVVDGAFFPNEPL 

391

331 270 271

271 332

211

WVQKNIEFFGGDPŚŚVTIFGESAGAISVSSLILSPMAKGLFHKAIMEŚGVAIIPYLEAHD

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                                                                                                                                                                Matches
                                                                                                                                                                                                                                This invention relates to novel drug metabolising enzymes (DME) and the nucleotide sequences which encode them. The invention may be useful for the development of compounds with a cytostatic, immunosuppressive, antiinflammatory, endocrine, ophthalmological, gastrointestinal or antisonist cativity acting as an agonist or antagonist of drug and treatment of disorders associated with decreased or increased include cancer, cell proliferative disorders, autoimmune/inflammatory, metabolising enzymes. Such disorders endocrine, eye, gastrointestinal (including liver disorders) and metabolic disorders. The present sequence is that of a human drug form part of the printed specification but was obtained in electronic formart from EDO
                                                                                                                                                                                                            Sequence 618
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 2; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human drug metabolizing enzymes, useful disorders associated with aberrant (DME) autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Azimzai Y,
Elliott VS
Lal P, Le
Ring HZ,
Walsh RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ring |
Walsh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-362498/39.
N-PSDB; ADR19681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-NOV-2000; 2000US-0252834P.
30-NOV-2000; 2000US-0250567P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INCY-) INCYTE GENOMICS
                                     151
                                                                                                                                                             491;
                                                                                      91
                                                                                                              31 GESAEGPORNTRIGWIOGKOVTVIGSPVDVNVFLGVPFAAPPLGSLRFTNPOPASFWDNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              i Y, Baughin MR
t VS, Gandhi AR
Lee EA, Lu DA:
12, Sanjanwala M
RT, Warren BA,
              PGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHABGNWAFKDQVAALS
                                                 RBATSYPNLCLONSBWLLLDOHMLKVHYPKFGVSBDCLYLNIYAPAHADTGSKLPVLVWF
                                                                                                                                                                      Similarity
PĠĠĀFKTĠŚĀŚĪFDĠŚĀĹĀĀŸĒDŸĹVVVVQŸRĹĠĪFĠFFTTWDQHĀFĠNWĀFKDQVĀĀĹŚ
                                                              84.1%;
ilarity 94.4%;
Conservative
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i AR,
l DAM,
a MS,
Xu
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Griffin JA, Hafalia AJA, Ison CH, K
Nguyen DB, Arvizu C, Policky JL, R
Tang YT, Tribouley CM, Narinder WK;
u Y, Yang J, Yao MG, Yue H;
                                                                                                                                                    Score 2588.5;
Pred. No. 9.6e.
1; Mismatches
                                                                                                                                              5; DB 5;
9.6e-233;
5;
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                                                                                                                                                 Indels
                                                                                                                                                                         618;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 and treatment cancer and
                                                                                                                                                 23;
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Ramkumar
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                        210
                                                 211
                                                                                                 151
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ADB64065
ID ADB64
XX Call
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                                                                                     The invention discloses a polymucleotide comprising a sequence selected CC from 1970 fully defined nucleotide sequences which encode novel CC polypeptides. Also claimed is a polypeptide encoded by the polymucleotide CC or its partial peptide, an antibody binding to the polypeptide or peptide CC of the polymucleotide, immunologically assaying the polypeptide or peptide CC peptide of the polymucleotide by contacting the polypeptide or peptide CC with the antibody of the encoded protein, and observing the binding CC between the two, a transformant carrying the polymucleotide in an CC expressible manner and an antisense polymucleotide. The oligonucleotide is useful as a primer for synthesising the polymucleotide, or as a probe CC for detecting the polymucleotide. The oligonucleotide CC genes may be included in them, for developing a diagnostic marker or CC medicines for regulation of their expression and activity, or as targets CC of gene therapy. The genes are involved in tissue and/or cell CC regeneration. Membrane proteins, signal transduction-related proteins, disease-related proteins and genes CC encoding them can be used as indicators for diseases (e.g. osteoporosis, cancer proteins, disease-related proteins and genes concounts them can be used as indicators for diseases (e.g. osteoporosis, the activity or expression of the encoded protein to treat diseases. The sequence data for this patent is not represented in the printed concern patent office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-450961/43.
N-PSDB; ADB62095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-NOV-2001;
25-JAN-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADB64065 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as targets of gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human protein encoded by clone
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RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page; 222pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISLWPAYNLTEQYLQLDLNMSLGQRLKEPRRDVWVTGYP 588
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2002US-00350978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Otsuki T, Wakamatsu A, Sato H, I
Hio Y, Otsuka K, Nagai K, Irie R,
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ishii S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tamechika I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
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Sequence 469

The present sequence represents a cat cauxin protein (I) or its salt, which is cat kidney disease marker. Also described: (1) a partial per (II) of (I); (2) a nucleic acid (III) encoding (I) or (II); (3) a vec

or (II); (3) a vector

Claim 3; SEQ ID NO 2; 33pp; Japanese.

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RESULT 11
ADF50145
ID ADF50
XX ADF50
XX ADF50
XX ADF50
XX Cat;
XX Cat;
XX JP200
XX JP200
XX JP200
XX O9-SE
XX O9-SE
XX O9-SE
XX O1-MA
XX (TOHO
DR WPI;
DR WPI;
DR WPI;
DR WPI;
DR N-PSD
XX N-PSD
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CC Which
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Best Local
                                                                              Novel cauxin protein or its salt, useful and for diagnosing cat kidney disease.
                                                                                                                                                                                          04-MAR-2002; 2002JP-00057908
                                                                                                                                                                                                                   04-MAR-2002; 2002JP-00057908
                                                                                                                                                                                                                                                 09-SEP-2003.
                                                                                                                                                                                                                                                                           JP2003250575-A
                                                                                                                                                                                                                                                                                                    Felis catus
                                                                                                                                                                                                                                                                                                                               cat; cauxin;
                                                                                                                                                                                                                                                                                                                                                          Cat cauxin protein SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                  ADF50145;
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADF50145 standard; protein; 542 AA
                                                                                                                                     2004-002277/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 MLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              473
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                                                                                                                        ADF50144.
                                                                                                                                                                TOHOKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAISVSSLILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHEC 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKGDIVMFEGATEEEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMS
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                                                                                                                                                                TECHNOARCH
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Pred. No. 2.4e-220;
""matches 0;
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                                                                                               Ωì
                                                                                               cat kidney disease marker,
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RESULT 12
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XX T2-200
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Best Local Simi
Matches 373;
             JP2003250575-A.
                                                                                    Cat cauxin protein SEQ ID
                                         Felis catus
                                                            cat; cauxin;
                                                                                                                 12-FEB-2004
                                                                                                                                             ADF50147;
                                                                                                                                                                   ADF50147 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IV) comprising (III); (4) a transformed host (V) comprising (III) or (IV); (5) producing (I) or (II) by culturing (V); (6) a antibody (VI) which couples specifically with (I) or (II); (7) diagnosing cat kidney of amount of (I) indicates presence of the disease; (8) a cat kidney of amount of (I) indicates presence of the disease; (8) a cat kidney measures the biological activity of urinary (I) or (VI); and (9) a cauxin detection kit which measures cauxin in a test sample. (I) is useful as a disease. (I) enables detection of cat kidney disease marker and (VI) is useful for diagnosting cat kidney correctly. (I) provides an early marker for the disease, and replaces blood testing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                            EGVPĹWPAYTQSEQYĹKĹĎĹSVSVGQKĹKĖQEVEFWNYTÍ
                                                                                                                                                                                                                                               NDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTI 549
                                                                                                                                                                                                                                                                         DTRPAFVKADHSDEIRFVFGGAFLKGDIVMFEGATEEEKLLSRKMRYWANFARTGDPNG
                                                                                                                                                                                                                                                                                          DTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKOMKYWATFARTGNPNG
                                                                                                                                                                                                                                                                                                                           LVADHYFYNKHŚPVBÍRDŚFĹDĹĹĠDVĹFVVPGVVTARYHRDÁGÁFVYFYBFQHPPQĊLN
                                                                                                                                                                                                                                                                                                                                         LVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALLTARYHRDAGAPVYFYBFRHRPQCFB
                                                                                                                                                                                                                                                                                                                                                                                            LDLLSQKAFKAIPSIIGVNNHECGFLLFMKEAPEILSGSNKSLALHLIQNILHIPPQYLH 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNATSYPKLCFOOLEWLVSYOHVLKVRYPKLEASEDCLYLNIYAPAHADNGSNLPVNVWF
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                                                              cat
                                                                                                              (first entry
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                                                     kidney disease marker; kidney disease
                                                                                                                                                                 protein;
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71.7%;
                                                                                     NO:4.
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Pred. No. 2.4e-176;
0; Mismatches 85;
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                                                                                                                                   CC The present sequence represents a cat cauxin protein (I) or its salt, CC (II) of (I); (2) a nucleic acid (II) encoding (I) or (II); (3) a vector (IV) comprising (III); (4) a transformed host (V) comprising (III) or (II) by culturing (V); (6) a antibody (VI) (CC which couples specifically with (I) or (III); (7) diagnosing cat kidney (CC of amount of (I) indicates presence of the disease; (8) a cat kidney (CC disease diagnostic agent comprising (I) abelling agent, a reagent which (CC detection kit which measures cauxin in a test sample. (I) is useful as a cC disease. (I) enables detection of cat kidney disease simply and court (CC correctly. (I) provides an early marker for the disease, and replaces (CC complicated diagnostic methods such as X-ray imaging, ultrasonic imaging, children (CC complicated diagnostic methods such as X-ray imaging, ultrasonic imaging, children (CC complicated diagnostic methods such as X-ray imaging, ultrasonic imaging,
                                   Best Local
Matches 37
                                                                         Query Match
                                                                                                       Sequence 542 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel cauxin protein or its salt, useful as a and for diagnosing cat kidney disease.
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                                   373;
                                                    Similarity
                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 4; 33pp; Japanese.
                          64.5%; Score 1985; DB 8; 71.7%; Pred. No. 2.4e-176; tive 60; Mismatches 85;
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                                                        Length 542;
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                        | LVANEYFHDKHSLITEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYBFRHRPQCFB
                                                                                                valltokáfnsvési igvnnhecafil-stefsei iggsnrslálylvhtelni ptoyih
                                                             GDÉRKKÓLÓVLÁRI CGCHÁSDSAÁLLOCLKAKÞSEELMDISKKLTFSI ÞVIDDFFFFÐEÞ
                                                                                                                                               DYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQXTKSFTRVVDGAFFPNEP
                                                                                                                                                                                    WVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIPYL-EAH
                                                                                                                                                                         WVRDNÍEFFGGDFRSVTÍFGESAGAÍSVSSLÍLSFIANGLFHKAÍMESGVAÍLFLLMRPP
                                                                                                                                                                                                            PĠĠĀFĸMĠŚĀŚSFDĠŚĀĹĀĀŸĒĎŸĹĪŸTTŎŸŖĹĠĨFĠFFDŤGĎĒHĀRĠŃŴĀLLĎŎŶĀĀĹT
                                                                                                                                                                                                                      PGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALS 210
                                                                                                                                                                                                                                                             REATSYPNICLQNSEWILLIDQHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVWF
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RESULT 13
ABP61006
ABP61006
AC ABP61
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KW antiinflammatory; cardiant; antiulcer; virucide; antithyroid;
KW cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;
KW wound healing disorders; atherosclerosis; Parkinson's disease;
KW Alzheimer's disease; autoimmune disorder; haematopoietic disorder;
KW Alzheimer's disease; autoimmune disorder; haematopoietic disorder;
KW cardiovascular disorders; pancreatitis; respiratory disorder;
KW hyperproliferation; systemic autoimmune disease; hyper-immunity;
KW developmental abnormality; gastrointestinal ulceration; neuropathy;
KW developmental disease; metabolic disease; sperm dysfunction;
KW thyroid disorder; hypothyroidism; brain damage; colitis;
KW thyroid disorder; hypothyroidism; brain damage; colitis;
KW angiogenesis; ovulation deficiency; neurological disease; stroke;
KW trachea; thymus; lymph node; muscular system; obesity; anorexia;
KW growth abnormality; precocious puberty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-DEC-2000; 2000US-0256710P.
20-DEC-2000; 2000US-0257048P.
09-JAN-2001; 2001US-0260482P.
30-JAN-2001; 2001US-0264922P.
06-FEB-2001; 2001US-0266797P.
19-MAR-2001; 2001US-0276988P.
04-APR-2001; 2001US-0281535P.
08-MAY-2001; 2001US-0289622P.
The invention relates to an isolated polypeptide with signal sequences which allow it to be secreted extracellularly or membrane associated. The activity of polypeptides of the invention may be described as, cytostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic, neuroprotective, immunosuppressive, haemostatic, antiinflammatory, cardiant, antiuleer, virucide, antithyroid, cerebroprotective, anorectic, and metabolic. Polypeptides and polynucleotides of the invention are useful in the treatment, or as a vaccine in the prevention of, cancer, wound healing disorders, infection, atherosclerosis, Parkinson's disease and Alzheimer's disease, autoimmune disorder, haematopoietic disorder,
                                                                                                                                                                                                                                                                                                                                                                                                             Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder.
                                                                                                                                                                                                                                                                                                                                                     Claim 1(a); Page 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-DEC-2001; 2001WO-US049232.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Martensen SA,
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DB; ABQ86171.
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Smith RF, St
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cardiovascular disorders, pancreatitis, respiratory disorder, hyperproliferation, systemic autoimmune disease, hyper-immunity, developmental abnormality, gastrointestinal ulceration, neuropathy, haematological diseases, metabolic diseases, sperm dysfunction, thyroid disorders e.g. hypothyroidism, brain damages, colitis, cone phototransduction deficiency, neurological diseases, stroke, angiogenesis, ovulation disorders, diseases in the spinal cord, thyroid gland, heart, trachea, thymus, lymph node and muscular system, obesity, anorexia, growth abnormalities, and alleviation of precocious puberty. The sequences given in records ABP60965-ABP61019 represent novel human proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammation, neoplastic diseases, nervous system related disorders
                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                  137
 317
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                                                                                     GATEEEKLLSRKMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPR
                                                                                                                                                                                                                       PBILSGSNKSLALHLIQNILHI PPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVP
                                                                                                                                                                                                                                                                                       PSKELLTLSQKTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPMKEA 361
                                                                                                                                                                                                                                                                                                                                                       ILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRTK
                                  VDFWTSTIPLILSASDMLHSPLSSLTFLSLLQPFFFFCAP
                                                                                                                                                        ALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFE
                                                                                                                                                                                                                                                                    PSKELLTLSQKTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPMKEA
                                                                                                                                                                                                                                                                                                                                      ILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRTK
VDFWTSTIPLILSASDMLHSPLSSLTFLSLLQPFFFFCAP
                                                                GATEEEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPR
                                                                                                                                  ALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFE
                                                                                                                                                                                                  PEILSGSNKSLALHLIQNILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVP
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                              57.8%; 50.
100.0%; Pr/
'''e 0;
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Pred. No. 2e-157;
                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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AAE20911 standard; protein; 561 A

AAE20911;

01-JUL-2002 (first entry)

Rat carboxylesterase-like enzyme protein.

RESULT 14
AABE20911
ID AABE20
XX AAE20
XX AAE20
XX O1-JU
XX RAt;
DT 01-JU
XX RAt;
CX RAT;
CA R Rat; carboxylesterase-like enzyme; organophosphorus intoxication; osteopathic; gene therapy; osteoporosis; antisense therapy; cytos detoxifying agent; Paget's disease; bone implant degradation; can dental implant; enzyme; gene expression.

Rattus ďB

WO200206454-A2

24-JAN-2002

10-JUL-2001; 2001WO-EP007919

17-JUL-2000; 2000US-0218564P

(FARB ) BAYER AG

Novel human carboxylesterase-like enzyme polypeptide, regulators of which are useful for preventing and treating organophosphorus intoxication,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Screening for agents which decrease or modulate the activity of carboxylesterase-like enzyme polypeptide. Carboxylesterase-like enzyme is compounds that increase the ability of human carboxylesterase-like enzyme decrease or modulate the activity of compounds that increase the ability of human carboxylesterase-like enzyme decrease. Such as organophosphorus intoxication, cancer and osteoporosis. Compounds that increase the ability of human carboxylesterase-like enzyme carboxylesterase-like enzyme decrease. Such as detoxifying agents. Compounds are useful as detoxifying agents. Compounds are useful as detoxifying agents. Comparticularly dental implants. Carboxylesterase-like enzyme is useful in composite assays for detecting diseases and antagonists are useful in composite assays for detecting diseases and abnormalities or mutations in the nucleic acid sequences which encode the enzyme. The coding sequence of carboxylesterase-like enzyme polynucleotide is useful conformations which specifically bind to mRNA transcribed from useful for modulating carboxylesterase-like enzyme gene expression. The present sequence is rat carboxylesterase-like enzyme gene expression. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 275
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                                                                                                    467
                                                                                                                                       407
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                                                                                                                                                                                                                      355 LLPM------KEAPEILSGSNKSLALHLIQNILHIPPQYLHLVANEYFHDKHSLTEIR
                                                                                                                                                                                                                                                                                                                                                         236 ISVSSLILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKSEDLQ-VVAHFCGNNASDSEAL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                  174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 VHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to a purified human carboxylesterase-like enzyme ypeptide. Carboxylesterase-like enzyme and its DNA are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 VHTPLGIPPAKPPVGPLRFAPPEPPEPPKSGVRDATSQPAMCLONLDILDEVGLLDMKMI- 115
LDLNMSLGQRLKEPRVDFWTSTIP 550
                                         VP-GSFFSGMKLDF---TEBERLLSRRMMKYWANFARQGNFNSBGLPYWFALDHDBQYLQ
                                                                                                                                     DSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRF
                                                              VFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTBQYLQ 526
                                                                                                              IQYTEMMGDFLFVIPALQVAHFQR-SHAPVYFYEFQHAPSYFKNVRPPHVKADHADEVPF
                                                                                                                                                                                  TIPMVMGTAQIIKE----LŚRENLQAVLKOTAAQMMLPPECGDLLMEEYMGNTDDSQTLQ
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                                                                                                                                                                                                                                                                                     LRCLRTKPSKELLTLSQKTKSETRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGF 354
                                                                                                                                                                                                                                                                                                                                TSVSSHVISPMSQGLFHGAİMESGVALLPDLIS---ETSETVSTTVAKLSGCEAMDSEAL
                                                                                                                                                                                                                                                                                                                                                                                                       VVTIÓYŘĹĠVLĠĖĖSŤGĎEHÁRĠNŃGYLDQVÄÄĹRŴVÓQNÍAHĖĠĠNĖNRVTĨĖĠĖSÄGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNVFLGVPFAAPPLGSLRFTNPOPASPWDNLREATSYPNLCLONSEWL----LLDQHWLK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPQG-LTSSASQWCFFLTLQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MPRNQĹHŚWLNAVLFGĹLĹ--ĹĹIHVQ-ĠQDSPES-SPIRTTHTĠQVQĠKLDHVKDTKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              561 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.0%; Score 1262.5; DB 5;
48.8%; Pred. No. 1.1e-108;
ative 77; Mismatches 179;
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521

Query Match Best Local Similarity

Matches

Conservative

91;

Score 1230; DB 3; Pred. No. 1.2e-105; 1; Mismatches 168;

Indels

24;

Gaps

90 æ

S

31 GPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAPPLGSLRFTNPQPASPWDNL

465

406 406

350

290

233

173

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Sequences AAF21614 - AAF22031 represent DNA sequences encoding human CC proteins AAB58711 - AAB59128. The DNA and protein sequences are CC associated with breast and ovarian cancer. Included in the invention are Sequences AAF22032 - AAF22040 and AAB59129 which are used in the convention. The breast and ovarian cancer associated DNA protein sequences of the CC invention. The breast and ovarian cancer associated DNA, protein, agonist concurrences exhibit cytostatic; immunosuppressive; nottinglation antiparasitic antialergic; hepatotropic; antidiabetic; continugal; antiparasitic and cardiant activity. The polynucleotide and CC antifungal; antiparasitic and cardiant activity. The polynucleotide and corest and ovarian cancer. The nucleic acid sequences, proteins, agonists confirmune disorders e.g. Addison's disease, prevention and treatment CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; cardiovascular disorders such as myocardial ischaemias; wound healing; infertious diseases such as cerebral anoxia and epilepsy; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            문
                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 1142-1144; 1299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-MAR-2000; 2000WO-US005881.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nnottropic; neurpprotective; antiviral; antiallergic; heartropic; antihiflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; addison's disease; allergy; autoimmune haemolytic anaemia; multiple sclerosis; rheumatoid arthritis; Crohn's disease; cardiovascular disorder; wound healing; neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; breast cancer; ovarian cancer; cytostatic;
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 549
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Gaps

59

483 NFARNGNPNGEGLPHWPLFDQEEQYLQLNLQPAVGRALKAHRLQFWKKALP 533	문
500 TFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIP 550	δ
427 EFQHQPSWLKNIRPPHMKADHGDELPFVF-RSFFGGNYIKFTEEEEQLSRXMMKYWA 482	₽
440 EFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWA 499	Ş
368 LLMLPPTFGDLLREEYIGDNGDPQTLQAQFQEMMADSMFVIPALQVAHF-QCSRAPVYFY 426	DЬ
380 ILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFY 439	ઇ
308 FLERHPQELLASADEQPVESIVGVNNNEFGWLIEKVMRIYDTQKEMDREASQAALQKMLT 367	DЪ
324 FFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPMKBAPEILSGSNKSLALHLIQN 379	ર્
252 LIASSADVISTVVANLSACDQVDSEALVGCLRGKSKEEILAINKPFKMIPGVVDGV 307	В
266 LEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGA 323	Ś
192 VAALRWVQQNIAHFGGNPDRVTIFGESAGGTSVSSLVVSPISQGLPHGAIMESGVALLPG 251	D <sub>P</sub>
206 VAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPWAKGLFHKAIMESGVAIIPY 265	Ş
132 VMVWIHGGALVFGWASLYDGSMLAALENVVVVIIQYRLGVLGFFSTGDKHATGNWGYLDQ 191	Вb
146 VLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVQYRLGIFGFFTTWDQHAPGNWAFKDQ 205	Ş
76 RDGTTHPAMCLQDLTAVESEFLSQFNMTFPSDSMSEDCLYLSIYTPAHSHEGSNLP 131	DЬ
91 REATSYPNICLQNSEWLLLDQHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLP 145	ঠ
16 GQDSASPIRTTHTGQVLGSLVHVXGANAGVQTFLGIPFAKPPLGFLRFAPPEPPESWSGV 75	В

Search completed: June 16, 2005, 20:41:52 Job time : 173 secs

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Copyright

GenCore version 5.1.6 (c) 1993 - 2005 Compugen

A33668 A57701 JC7990 A34967

sterol esterase (E sterol esterase (E acetylcholinestera

sterol esterase (E

JE0150

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Result
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Maximum Match 100%
Listing first 45 s
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Maximum DB
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Perfect score:
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seq length: 2000000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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3079
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  Length
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1300.045 Million cell
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                                                                                                                                                                                                                                                                                                   Description
                                                                                                  acetylcholinestera
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A47162

thiolesterase B (EC 3.-.-) precursor - mallard c;species: Anas platyrhynchos (mallard)
C;species: Anas platyrhynchos (mallard)
C;pate: 05-May-1995 #sequence_revision 05-May-1995
C;Accession: A47162
R;Hwang, C.S.; Kolattukudy, P.E.
J. Biol. Chem. 268, 14278-14284, 1993
J. Biol. Chem. 268, 14278-14284, 1993
A;Title: Molecular cloning and sequencing of thioes A;Teference number: A47162; MUID:93300823; PMID:831
A;Accession: A47162
A;Status: preliminary
A;Molecula type: mRNA
A;Residues: 1-557 - HWA>
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                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q04791; GB:L05493; NID:g213100; PIDN:AAA49223.1; PID:g213101 (;Superfamily: cholinesterase; Cholinesterase homology C;Keywords: hydrolase C;Keywords: hydrolase F;56-545/Domain: Cholinesterase homology <CHE>
                                                           밁
                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 265
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                                                                                                                                                                                                                                                            23
                                                                                                                                                                                                                                                                               30
                                                                                                                                                                                                                                                                                                              Similarity
                                  LHI----PPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAP
                                                                             GAFFPNBPLDLLSQKAFKAIPSIIGVNNHECGFLLP-MKEAPEILSGSNKSLALHLIQNI
                                                                                                                                                   | QVAALSWVQKNIBFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAI-I
                                                                                                                                                                             PVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKD
                                                                                                                                                                                                                                  LREATSYPNLCLQNSEWLLLDQHML-----KVHYPKFGVSEDCLYLNIYAPAHADTGSKL
                                                                                                                                                                                                                                                           TGOKAEQPEVVTNYGSVRGYQVKVNAABRSVNVFLGLPFAKPPVGPLRFSEPQPPEPWKG
   VYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKVM
                    LFTE----QPEEQAQRIAAAAGCEKSSSAALVECLREKTEAEMEQITLKMPPMFISASLD
                                                                                                                     PYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKEL--LTLSQKTKSFTRVVD
                                                                                                                                                                                                                   VRDAASYPPMCLQDK---VLGQYLSDAITNRKEKVRLQISEDCLYLNVYTPVSTEEQEKL
                                                                                                                                                                                                                                                                      TGPSAEGPORNTRIGWIOGKQVTVLGSPVPVNVELGVPFAAPPLGSLRFTNPQPASPWDN
                                                            GVFFPKSPROLLSEKVINÁVPYIIGVNNCEFGWILPRMMKFPEFTEGLEKDVÁRQVLQST
                                                                                                                                        QVAALQWIQENIIHFRGDFGSVTIFGESAGGVSVSALVLSPLAKGLFHKAISESGTAVRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.2%; Score 1298.5; DB ilarity 48.4%; Pred. No. 4.1e-94; Conservative 79; Mismatches 177
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T37254
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A25363
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                                                                                                                                                                                                                                                                                                     177;
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esterase - Caenorh
protein B0238.1 [i
triacylglycerol li
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crystal protein pr
acetylcholinestera
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carboxylesterase (
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acetylcholinestera
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Gaps

8

82

139 144

204

321

435

263 199

259

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R;Ozols, J.

J. Biol. Chem. 264, 12533-12545, 1989
A;Title: Isolation, properties, and the complete amino aci
A;Reference number: A34329; MUID:89308686; PMID:2745458
A;Accession: A34329
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-532 <020>
A;Cross-references: UNIPROT:p14943
C;Superfamily: cholinesterase; cholinesterase homology
F;32-517/Domain: Cholinesterase; CHE>
F;32-517/Domain: Cholinesterase complete amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60K esterase (EC 3.1.1.-) isoform 2 - rabbit C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 C;Accession: A34329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
A34329
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201,430/Active site: Ser, His #status predic
                                                                                                                502
                                                                                                                                                                                                     355 -- PPALGDĹLMDEÝNGSNEDPKHLMAQFQEMMAĎAMFÝMPÁĽRVÁHLQR-SHÁPTYFÝEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 LTMGMÁŚMYDĠŚAĹAAFEDVVVVTIQYRĹGVLGFFSTGDQHÁTGNHGYLDQVAAĹRWVQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155
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                                                                                                                                                      RHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFBGATBBEKLLSRKMMKYWATF
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                                                           ARNRNPNGEGLAHWPLFDLDQRYLQLNMQPAVGQALKARRLQFWTHTLP
                                                                                          ARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIP 550
                                                                                                                              QHRPSFTKDLRPPHVRADHGDEVVFVFRSHLFGSKVPL----TEEEELLSRRVMKYWANF
                                                                                                                                                                                                                                                                              LADFQPVPSIIGINNDEYGWIIPKLLLAIDPQBERDRQAMREIMHQATKQLML-----
                                                                                                                                                                                                                                         HIPPOYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVVFYEF
                                                                                                                                                                                                                                                                                                                OKAFKAIPSIIGVNNHECGFLLP-------MKEAPEILSGSNKSLALHLIQNIL
                                                                                                                                                                                                                                                                                                                                                   S--TVVANLSRCGQVDSETLVRCLRAKSBEEMLAITQVFMLIPGVVDGVFLFRHFEELLA
                                                                                                                                                                                                                                                                                                                                                                                       EDLQVVAHFCGNNASDSBALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFENEPLDLLS 334
                                                                                                                                                                                                                                                                                                                                                                                                                            NIAHFGGNÞGRVTÍFGESÁGGTSVSSHVLSÞMSQGLFHGAIMESLVALLÞGLITSSSEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALSWVQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAMCLÓN -- LAIMDÓDVÍLLHFTPÞSIPMSEDCLÝLNÍÝSÞÁHÁRBÓSDÍÞVMVWIHGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PNLCLQNSEWLLLDQHWLKVHY--PKFGVSEDCLYLNIYAPAHADTGSKLPVLVWFPGGA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIŔNTHTĠQVRĠSLVHVEĞTDAGVHTFLĞIPFÂKPPLĞPLRFAPPEPÂBAWSGVRDGTSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PORNTRLGWIQGKOVTVLGSEVEVNVELGVEFAAPPLGSLRETNPQPASEWDNLREATSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KYWTNFÄRNGNFNGEGLVHWPQYDMDERYLEIDLTQKAAKKLKERKMEFWMQLTEQIMSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KYWATFARTGNPNGNDLSLWPAYNLTBOYLOLDLNMSLGQRLKEPRVDFWTSTIPLILSA 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||||||:|||
|VYFYEFQHRPSSAAGVVPEFVKADHADEIAFVFGKDFLAGN-----
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47.8%; Pre
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Pred. No. 7.26
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carboxylesterase (EC 3.1.1.1) precursor - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 26-Dec-1994 #sequence_revision 03-Aug-1995 #text
C;Accession: S47655
                                                                                  RESULT
S47655
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C;Superfamily: cholinesterase; cholinesterase homology
C;Kupwords: carboxylic ester hydrolase; glycoprotein
F;58-544/Domain: cholinesterase homology <CHE>
F;159-5123-280,291-428/Disulfide bonds: #status predicted
F;111,276/Binding site: carbohydrate (Asn) (covalent) #status
F;228,457/Active site: Ser, His #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:000748; GB:Y09616; NID:92058317; A;Experimental source: intestine C;Comment: This enzyme hydrolyzes many xenobiotics, such as C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ryschwer, H.; Largmann, T.; Daig, R.; Becker, A.; Aslanidis, C.; Schmitz, G. Blochem. Blophys. Res. Commun. 233, 117-120, 1997
A;Title: Molecular cloning and characterization of a novel putative carboxylesterase, A;Reference number: JC5408; MUID:97289502; PMID:9144407
A;Accession: JC5408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-559 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Experimental source: intestine
;Comment: This enzyme hydrolyzes many xenobiotics, such as carboxyl esters,
                                                                                                                                                          493
                                                                                                                                                                                             500
                                                                                                                                                                                                                                 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 REATSYPNICLON-----SEWLLLDQHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31
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                                                                                                                                                                           TFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIP
                                                                                                                                                                                                                   EFQHQPSWLKNIRPPHMKADHGDELPFVF-RSFFGGNYIKF--
                                                                                                                                                                                                                                             EFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWA
                                                                                                                                                                                                                                                                                      LIMIPPTFGDLLREEYIGDNGDPQTLQAQFQEMMADGNFVIPALQVAHF-QCSRAPVYFY
                                                                                                                                                                                                                                                                                                                        ILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFY
                                                                                                                                                                                                                                                                                                                                                           FLPRHPQELLASADFQPVPSIVGVNNNEFGWLIPKVMRIYDTQKEMDREASQAALQKMLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ĻEAHDYEKSEDL--QVYAHFCGNNASDSEALLRÇLRTKPSKELLTLSQKTKSFTRVYDGA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                   FFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLD----MKEAPEILSGSNKSLALHLIQN
                                                                                                                                                                                                                                                                                                                                                                                                                                    ĹIĀ----SŚAĎVISTVVÁNLSACDQVĎŠEAĹVGČĽRGKSKEBILAINKPFKMIPGVVĎGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAALRWVQQNTAHFGGNFDRVTTFGESÄGGTSVSSLVVSFISQGLFHGAIMESGVALLFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VMVWIHGGALVFGMASLYDGSMLAALENVVVVIIQYRLGVLGFFSTGDKHATGNWGYLDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GESAEGPORNTRIGWIQGKOVTVLGSPVPVNVFLGVPFAAPPLGSLRFTNPQPASPWDNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLVWFFGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RDGTTHPAMCLQDLTAVESEFL----SQENMTFPSDSMSEDCLYLSIYTPAHSHEGSNLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GQDSASPIRTTHTGQVLGSLVHVKGANAGVQTFLGIPFAKPPLGPLRFAPPEPPESWSGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.9%; Score 1230; DB 1; 46.7%; Pred. No. 1e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1e-8
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 559;
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24;

Gaps

thioesters PID: 9205831

pre

85

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#text\_change

09-Jul-2004

436 439

379 377

317

261

201 205 141

F;215,443/Active site: Ser, His #status predicted

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RESULT 5
$34607
$34607
$carboxylesterase (EC 3.1.1.1) - mouse
$C;Species: Mus musculus (house mouse)
$C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
$C;Accession: S34607
$R;Aida, K.; Moore, R.; Negishi, M.
Biochim. Biophys. Acta 1174, 72-74, 1993
$A;Title: Cloning and nucleotide sequence of a novel, male-predominant carboxyleste
$A;Reference number: S34607; MUID:93326638; PMID:7916639
$A;Accession: S34607
$A;Status: preliminary
$A;Accession: S34607
$A;Cross-reference: UNIPROT:063880; GB:S64130; NID:9404388; PIDN:AAB27606.1; PID:
$C;Superfamily: cholinesterase; cholinesterase homology
$C;Superfamily: cholinesterase; cholinesterase homology
$C;Reywords: carboxylic ester hydrolase
$C;Reywords: carboxylic ester hydrolase
$C;Reymords: carboxylic ester hydrolase
$C;Reymords: carboxylic ester hydrolase
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Biochim. Biophys. Acta 1207, 118-142, 1994
A;Title: Cloning and sequence analysis of a hamster liver cDNA encoding
A;Reference number: S47655; MUID:94318665; PMID:8043605
A;Accession: S47655
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C;Superfamily: cholinesterase; cholinesterase
C;Keywords: carboxylic ester hydrolase
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A;Molecule type: mRNA
A;Residues: 1-561 <SON>
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEF
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47.3%; Pred. No. 2.8e-86;
tive 74; Mismatches 181;
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RESULT 6
A39060
carboxylesterase (EC 3.1.1.1) precursor -
C;Species: Mus musculus (house mouse)
C;Date: 06-Mar-1992 #sequence_revision 06-
                                                          A;Cross-references: UNIPROT:P23953; GB:M57960; NID:g192853; PIDN:AAA63297.1; PID:g192854 C;Superfamily: cholinesterase; cholinesterase homology C;Keywords: carboxylic ester hydrolase F;50-540/Domain: cholinesterase homology <CHE>F;221,455/Active site: Ser, His #status predicted
                                                                                                                                                                                                                                               C;Accession: A39060
R;Ovnic, M.; Tepperman, K.; Medda,
Genomics 9, 344-354, 1991
                                                                                                                                                                              A;Title: Characterization of a murine cDNA
A;Reference number: A39060; MUID:91169540;
A;Accession: A39060
A;Status: preliminary
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A; Residues: 1-554 < OVN>
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Similarity 46.5%;
                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALITARYHRDAGAPVYFYBFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFL--KGDIVM 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KAIMESGVAIIPYLEAHDYEKSEDLQVVAH--FCGNNASDSEALLRCLRTKPSKELLTLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLIFSKYLQDAGCPVFLYEFQHTPSSFAKFKPAWVKADHSSENAFVFGGPFLTDESSLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVNISYT--VNDSFFPQRPQKLLANKQFPTVPYLLGVTNHEFGWLLLKFWNILDKMEHLS
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Conservative
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               37.8%; Score 1163; DB 2; 44.3%; Pred. No. 1.9e-83;
 84; Mismatches 193;
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PMID:1840565
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                                                                                                                                                                                                                                                                 D.A.; Grant,
                                                                                                                                                                                                                                     carboxylesterase
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16

LILQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAPPLGS

75

Gans

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F;19-566/Product: carboxylesterase #status experimental <MAT>
F;51-552/Domain: cholinesterase homology <CHE>
F;80/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;222,467/Active site: Ser, His #status predicted
                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Molecule type: protein
A;Residues: 19-40 <MAT2>
A;Note: 28-Lys and 33-Leu were also found
C;Superfamily: cholinesterase; cholinesterase homology
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum;
F;1-18/Domain: signal sequence #status predicted <SIGs
F;1-18/Domain: signal sequence #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
S19307
Carboxylesterase (EC 3.1.1.1) precursor - pig
N;Alternate names: proline-beta-naphthylamidase
C;Species: Sus scrofa domestica (domestic pig)
C;Accession: S19307; S23607
R;Matsushima, M.; Inoue, H.; Ichinose, M.; Tsukada, S.; Miki, K.; Kurokawa, K.; Takahash
A;Title: The nucleotide and deduced amino acid sequences of porcine liver proline-beta-r
A;Recression: S19307; MUID:92070571; PMID:1959668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-566 < MAT1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;CTOSS references: UNIPROT:Q29550; EMBL:X63323; NID:g1930; PIDN:CAA44929.1; PID:g1931
                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                              Local Similarity
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                                                                                      WCFFLILOPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAP 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183
                                               Wilpivítsíassatm--agopaspþvvdtaogrvlgkyvsleglaopvavelgvþfakþ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEETAŠĹLĹRRFHSELNÍSESMIPAVIEQÝLRGVDDPAKKSELIĹDMFĠĎIFFGIPAVLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VÓYNIŠLSTMIDĠVVLĖKAPEBILAEKSPNTVPYĪVĞFNKQĖFĠWIIPMLQNLLPEGKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -QKTKSFTRVVDGAFFPNBFLDLLSQKAFKAIPSIIGVNNHECGFLLPM---KEAPE-IL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPADLTKSSQLÞÝMÝMIHGGGLVIGGRSÞYNGLÁLSÁHENÝVÝVTIQÝRLGIMGLFSTGÐ
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                                                                                                                                                     37.8%; Score 1162.5; DB 2; 44.3%; Pred. No. 2.1e-83; tive 71; Mismatches 202;
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A;Accession: JX0054

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R;Takagi, Y.; Moroh
J. Biochem. 104, 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carboxylesterase (EC 3.1.1.1) El precursor, minor form - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_charcarana...vanc.
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YLNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGF 188
                                               LRFAPPEPABPWSFVKNTTTYPPMCSQDGVVGKLLADMLSTGKESIPLEF----SEDCL
                                                                                        LRFTNPOPASPWDNLREATSYPNLCLQN-----SEWLLLDQHMLKVHYPKFGVSEDCL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235
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                                                                                                                                             LAVCPIWĠĤ-----PŚSP-PVVDŤTKĠKVLĠŔYVSLEĠFTQPVAVFĹĠVĒFĀKPPĹĠS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RDSLLDLLGDVEFVVPALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVR 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELLTLSQKTKSFT------RVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNN 349
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                                                                                                                                                                                                                                                   37.2%; Score 1144; DB 2;
43.5%; Pred. No. 5.8e-82;
htive 92; Mismatches 183;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         550
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34;

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412 405

234 244 174 184 114 124

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A41010
carboxylesterase (BC 3.1.1.1) precursor, monocyte/macrophage [validated] - human
N;Alternate names: carboxylesterase, hepatic; monocyte/macrophage serine esterase
C;Species: Homo sepiens (man)
C;Date: 10-Sepiens) Heequence, revision 10-Sep-1999 #text change 09-ul-2004
C;Accession: A41010; JH00277; A47916; A49816; P80280; I61085; A48809; U57004
R;Munger: JS.; Shi, G.P.; Mark, E.A.; Chin, D.T.; Gerard, C.; Chapman, H.A.
J;Biol. Chem. 266, 18832-18838, 1991
A;Title: A serine esterase relassed by human alveolar macrophages is closely related to A;Reference number: A41010
A;Molecule type: mRNA
A;Residues: 1-567 AUMUs
A;Reference number: JH0327; MJD:91148424; PMID:917927; PIDN:AAA35649.1; PID:9179928
A;Note: parts of this sequence, including the amino end of the mature protein, were conf
R;Long, R.M.; Calabrees, M.R.; Martin, B.M.; Pohl, L.R.
A;Title: Cloning and sequencing of a human liver carboxylesterase isoenzyme.
A;Reference number: JH0327; MJD:91148424; PMID:917784
A;Accession: JH0327; MJD:91148424; PMID:997784
A;Accession: A47376; MJD:91148424; PMID:997784
A;Accession: A47376; MJD:910804043; PMID:91080650.1; PID:9179930
A;Title: Nolecular Cloning and characterization of a human carboxylesterase gene.
A;Reference number: A47376; MJD:910913; PMID:9406473
A;Accession: A47376
A;Accession: A47376
A;Accession: A47376
A;Accession: A620198; NID:9455476; PIDN:BAA04650.1; PID:9458470
A;Accession: A620198; NID:9455476; PIDN:BAA04650.1; PID:9458470
A;Accession: A4916
A;Accession: A4936
A;A
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                LFLDLIADVMFGVPSVIVARNHRDAGAPTYMYEFQYRPSFSSDMKPKTVIGDHGDELFSV
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A;Cross-references: GB:X52973; NID:g36421; PIDN:CAA37147.1; PID:g1335304 R;Riddles, P.W.; Richards, L.J.; Bowles, M.R.; Pond, S.M. Gene 108, 289-292, 1991 Gene 108, 289-292, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;146-567/Product: carboxylesterase #status experimental F;564-567/Region: endoplasmic reticulum retention signal F;221,468/Active site: Ser, His #status predicted
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A;Map position: 16q13-16q22.1
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum;
F;1-18/Domain: signal sequence #status predicted <SGS
F;19-145/Domain: propeptide #status predicted <PRO>
F;19-145/Domain: cholinesterase homology <CHE>
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Biochemistry 32, 11606-11617, 1993
A;Title: Glycosylation-dependent activity of baculovirus-expressed human liver carboxyles A;Reference number: A48809; MUID:94032283; PMID:8218228
A;Recession: I51085
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A;Cross-references: GB:M65261; NID:g187028; PIDN:AAA83932.1; PID:g187029
A;Experimental source: liver
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A;Residues: 1-17,'A',18-55,'G',57-535,'G',537-567 <KRO2>
A;Cross-references: GB:L07764; NID:g180947; PIDN:AAA16036.1; PID:g180948
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A;Residues: 1-55,'G',57-361,363-535,'G',537-567 <KROl>
A;Cross-references: GB:L07765; NID:g180949; PIDN:AAA35711.1;
A;Accession: A48809
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Local Similarity 44.3%;
SLLDLLGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WCFFLILQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAP 71
                                                                                                                                                    GWLIPMQLMSYPLSEGQLDQKTAMSLLWKSYPLVCIAKELIPEATEKYLGGTDDTVKKKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKG 249
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Pred. No. 1.3e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -RVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHEC
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A;Accession: A55304
A;Nolecule type: mRNA
A;Residues: 1-6, (°, 8-59, °P', 61-212, 'A', 214-252, 'T', 254-309, 'IT', 312-341, 'N', 343-424, 'FY
A;Cross-references: GB:U10697; NID:g562007
A;Note: the sequence in GenBank entry RNU10697, release 107, (PID:g562008) has the codor R;Robbi, M.; Beaufay, H.
submitted to the EMBL Data Library, September 1994
A;Reference number: S49257
A;Accession: S49257
A;Accession: S49257
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A;Residues: 1-561 <RO2>
A;Cross-references: EMBL:X81825; NID:g550417; PIDN:CAA57419.1; PID:g550418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 19-48 <MOR>
A;Esperimental source: liver
A;Experimental source: liver
R;Yan, B.; Yang, D.; Brady, M.; Parkinson, A.
J. Biol. Chem. 269, 29688-29696, 1994
A;Title: Rat kidney carboxylesterase. Cloning, sequencing, cellular localization, A;Accession: A55304; MUID:95050819; PMID:7961958
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$62788
Carboxylesterase (EC 3.1.1.1) ES-4 precursor, liver - rat
N;Alternate names: hydrolase B
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1996 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: $62788; S51203; A55304; $49257
R;Robbi, M: van Schaftingen, E: Beaufay, H.
Biochem J: 313, 821-826, 1996
A;Title: Cloning and sequencing of rat liver carboxylesterase ES-4 (microsor A;Reference number: $62788; MUID:96190723; PMID:8611161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Morgan, E.W.; Yan, B.; Greenway, D.; Petersen, D.R.; Parki
Arch. Biochem. Biophys. 315, 495-512, 1994
A;Title: Purification and characterization of two rat liver
A;Reference number: S51202; MUID:95077430; PMID:7986098
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A;Residues: 1-561 <ROB>
A;Cross-references: UNIPROT:Q64573; EMBL:X81825; NID:g550417;
A;Experimental source: 11yer
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                                62
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                                SLRFTNPQPASPWDNLREATSYPNLCLQNSEW-----LLLDQHMLKVHYPKFGVSEDCLY
                                                                                                                       FLILQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVELGVPFAAPPLG
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      SLRFAPPÓPABPWSFVKNTTTYPPMCSÓDAAKGORMNDLLTNRKEKIH---LEFSEDCLY
                                                                                    PĹĬĹVSĹATCVVYĠ--NPŚSP-PVVDTTKĠKVLĠKYVSLEGVTQSVAVFĹĠVPFAKPPLĠ
                                                                                                                                                                         37.0%; Score 1139; DB 2; ilarity 43.4%; Pred. No. 1.5e-81; Conservative 82; Mismatches 195;
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                                                                                                                                                                                                              Length 561;
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A;Molecule type: mRNA; protein
A;Residues: 1-562 < OVN>
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A55281
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Matches 240
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410 LDLLGDVEFVVPALITARYHRDAGAPVYEYEFRHRPQCFEDTKPAFYKADHADEVRFYFG
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                                                                                        GAFLKGDIVMFEGATEEEKLLSRKMMKYWATFARTGNPNGNDLSLWFAYNLTEQYLQLDL 529
TTQQSQRLKAEEVAFWTQLL 549
                                   NMSLGQRLKEPRVDFWTSTI 549
                                                             APIĹR-----DĠÁSBĖBIKĹŚKMVMKFWANFARNGNĖNGRGĹPHWĖQYDQKĖBYLQIGA 529
                                                                                                                                        LAFTĞDVSFSIPSVMVSRDHRDAĞAPTYMYBYQYYPSFSSPQRPKHVVGDHADDLYSVFG
                                                                                                                                                                                                                                                                                                  MKKOMLIKLSSQRDNKESYHFLSTVVDNVVLPKDPKEILABKNENTVPYİVĞINKQECGW
                                                                                                                                                                                                                    LLPTMMGFVPADVE-LDKKMÄTTLLEKFASLYGİPEDIIPVAIEKYRKGSDDSIKIRDGI
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                                                                                                                                                                                                                                                                                                                                      SQKTK-----SFTRVVDGAFFPNBPLDLLSQKAFKAIPSIIGVNNHECGF
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Carboxylesterase (BC 3.1.1.1) egasyn - mouse
N;Alternate names: beta-glucuronidase endoplasmic reticulum-targeting protein; esterase-;
C;Bpecies: Mus musculus (house mouse)
C;Date: 10-Feb-1995 #sequence\_revision 10-Feb-1995 #text\_change 09-Jul-2004
C;Accession: A55281
R;Ovnic, M.; Swank, R.T.; Fletcher, C.; Zhen, L.; Novak, E.K.; Baumann, H.; Heintz, N.; (Genomics 11, 956-967, 1991
Genomics 11, 956-967, 1991
A;Reference number: A55281; MUID:92147141; PMID:1783403
A;Accession: A55281

PID: 9244728

37.0%; Score 1138.5; DB 2; 44.4%; Pred. No. 1.6e-81; ative 76; Mismatches 195; Length 562;

209 LSWVQKNIEFFGGDFSSYTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIFYLEA KNATSYPPMCFQDPVTGQIVNDLLTNRKEKIPLQPSEDČLYLNIYTPADLTKSDRLPVMV REATSYPNLCLQNSEWLLLDQHMLKVHYPKFGV--SEDCLYLNIYAPAHADTGSKLPVLV GPSAEGPORNTRIGWIOGKOVTVIGSPVPVNVFIGVPFAAPPIGSIRFTNPOPASPWDNI 90 GHPSSPPMVDTVQGKVLGKYISLEGFTQPVAVFLGVPFAKPPLGSLRFAPPQFAEPWSSV 78 Conservative Indels 29; Gaps 208 198 138 148

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A;Cross-references: UNIPROT:P10959; GB:M20629; GB:X13587; NID:g203279 C;Superfamily: cholinesterase; cholinesterase homology C;Superfamily: cholinesterase; cholinesterase homology C;Keywords: carboxylic ester hydrolase; glycopretein F;1-9/Domain: signal sequence #status predicted <SIG> F;10-540/Product: carboxylesterase #status predicted <MAT> F;10-540/Product: carboxylesterase #status predicted <MAT> F;10-520/Domain: cholinesterase homology <CHE> F;70,265,266,293,366,467/Binding site: carbohydrate (Asn) (covalent) F;212,444/Active site: Ser, His #status predicted
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-May-1990 #sequence_revision 03-Aug-1992 #text_change 09-Jul-2004
C;Accession: A31584
R;Long, R.M.; Satoh, H.; Martin, B.M.; Kimura, S.; Gonzalez, F.J.; Pohl, L.R.
Biochem. Biophys. Res. Commun. 156, 866-873, 1988
A;Title: Rat liver carboxylesterase: cDNA cloning, sequencing, and evidence fa;Reference number: A31584; MUID:89050119; PMID:2973315
A;Accession: A31584
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A; Residues: 1-540 <LON>
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                                                                                                                                                                                                                                                                                                                                                    YLNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGF 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LILOPLIGHROWGKTGPSAEGPORNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAPPLGS
                                                                                                                   NLFHRAISESGVVLTTNLDKKNTQAV--AQMIATLSGCNNTSSAAMVQCLRQKTEAELLE
                                                                                                                                                               GLFHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLT 308
                                                                                                                                                                                                                                                       FTTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAK 248
                                                                                                                                                                                                                                                                                                          YLNIYSPADLTKNSRLPVMVWIHGGGLIIGGASPYSGLALSAHENVVVVTIQYRLGFGGL 168
                                                                                                                                                                                                                                                                                                                                                                                                     LRFAPPEPAEPWSFVKNTTTYPPMCSQDGVVGKLLADMLSTGKESIPLEF-----SEDCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAVCPIWGH-----PSSP-PVVDTTKGKVLGKYVSLEGFTQPVAVFLGVPFAKPPLGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSRKWMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RDAGAPTYMYEFQYSPSFSSEMKPDTVVGDHGDEIYSVFGAPILRG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKL 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALHLIQN----ILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---TRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLP-MKEAPEILSGSNKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNTRPLAEKIAVISGCKN--TTSAAMVHCLRQKTEEELLGTTLKLNLFKLDLHGDSRQSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HDYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSF------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LHWVQDNIAKFGGDPGSVTIFGESAGGESVSVLVLSPLAKNLFQRAISESGVALTAGLVK
                        LTVKLDNTSMSTVIDGVVLPKTPEEILTEKSFNTVPYIVGFNKQEFGWIIPTMMGNLLSE 346
                                                                  LSOK--TKSFTRVVDGAFFPNEPLDLLSOKAFKAIPSIIGVNNHECGFLLPMKEAPBILS 366
                                                                                                                                                                                                             FSTGDEHSRGNWAHLDQLAALRWVQDNIANFGGNPDSVT1FGESAGGVSVSALVLSPLAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMSLLKKSSFLLNLPEDAIAVAIEKYLRDKDYTGRNKDQLLELIGDVVFGVPSVIVSRGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.9%; Score 1136; DB 2; ilarity 43.3%; Pred. No. 2.4e-81; Conservative 91; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GB:X13587; NID:g203279; PIDN:AAA40871.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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F;50-551/Domain: cholinesterase homology <CHE>
F;558-561/Region: endoplasmic reticulum retention signal
F;79,301/Binding site: carbohydrate (Asn) (covalent) #status
F;221,466/Active site: Ser, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Title: Cloning and expression of hydrolase C, a member A.Reference number: S71597; MUID:95177656; PMID:7872788 A.Accession: S71597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: cholinesterase; cholinesterase homology C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum; F;1-18/Domain: signal sequence #status predicted <SIG> F;19-561/Product: carboxylesterase #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-561 < YAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carboxylesterase (EC 3.1.1.1) precursor, liver - rat

N,Alternate names: hydrolase C

C;Species: Rattus norvegicus (Norway rat)

C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 13-Sep-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: liver; endoplasmic reticulum C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: S71597
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                                                                                                                                                                                                                                                              VAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIPY 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                             REATSYPNICLQNSEW-----LLLDQHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPSAEGPQRNTRLGWIQGXQVTVLGSPVPVNVFLGVPFAAPPLGSLRFTNPQPASPWDNL
                                                                                                                                                                                                                                                                                                                                                                             VLVWFPGGAEKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQ 205
                                                                                                                                                                                                                                                                                                                                                                                                                              KNTTTYPPMCSQDATKGQRMNDLLTNRKEKVH----LQFSEDCLYLNIYTPADFTKDSRMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DFWTSTI 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEG 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G-SNKSLALHLIONI---LHIPPOYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPA 422
NKSLALHLIQ---NILHIPPQYLHLVANEYFHDKHSLTBIRDSLLDLLGDVFFVVPALIT
                                                                                             S----FTRYVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLP--MKEAPEILSGS
                                                                                                                                                                                       LEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQK-----TK 314
                                                                                                                                                                                                                                                                                                                                   VMVWIHGGGLTQGGASTYDGRVLSAYENVVVVAIQYRLGIWGFFSTGDEHSRGNWGHLDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNPSSPPVVDTMKGKVLGKYASLEGVTQSVAVFLGVPFAKPPLGSLRFAPPQPAEPWSFV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFWTELL 527
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                                                                                                                                           LFTKDVRPA--AKQIADMAGCKTTTSAIIVHCLRQKTEEELLEIMEKMNLIKLSSQRDTK
                                                                                                                                                                                                                                      VAALHWVQDNIANFGGDPGSVTIFGESAGGFSVSVLVLSPLSKNLYHRAISESGVVLITQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLMSRSLRDAGAPTYMYEFQYRPSFVSDQRPQTVQGDHGDEIFSVFGTPFLK-----EG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.7%; Score 1129.5; DB 2; 43.4%; Pred. No. 8.3e-81; tive 83; Mismatches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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A; Molecule type: mRNA
A; Residues: 503-554, 'R', 556-561 <MED>
A; Cross-references: EMBL: X65295; NID: 957557; PIDN: CAA46390.1; PID: 957558
C; Superfamily: cholinesterase; cholinesterase homology
C; Keywords: carboxylic ester hydrolase; glycoprotein
F; 11-8/Domain: signal sequence #status predicted <SIG>F; 11-561/Product: carboxylesterase ES-3 #status predicted <MAT>
F; 50-551/Domain: cholinesterase homology <CHE>
F; 79, 107, 489/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 221, 466/Active site: Ser, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Medda, S.; Proia, R.L.
Eur. J. Biochem. 206, 801-806, 1992
A;Title: The carboxylesterase family exhibits C-terminal A;Reference number: $23460; MUID:92299008; PMID:1606962
A;Accession: $23462
A;Status: preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carboxylesterase (EC 3.1.1.) ES-3 precursor - rat C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Mar-1995 #sequence_revision 26-May-1995 #text_chang.
C;Accession: JC2447; S23462
R;Robbi, M; Beaufay, H.
Biochem. Biophys. Res. Commun. 203, 1404-1411, 1994
A;Title: Cloning and sequencing of rat liver carboxylesterase A;Accession: JC2447; MUID:95032008; PMID:7945287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-561 <ROB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
JC2447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: UNIPROT:Q63108; GB:X81395; NID:g550146; PIDN:CAA57158.1; PID:g55014:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                        242
                                                                                                                                                                                                                       182 RLGIFGFFTTWDQHADGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSL 241
                                                                                                                                                                                                                                                                                                            122 GVSEDCLYLNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQY
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                                                                KPSKELLTLSQKTKSFT-.
                                                                                          VLSPLAKNI.FHKAISESGVALTAGLVKKNTRPLAEKIAVVS---GCKSTTSASMVHCLRQ
                                                                                                                                    ILSPMAKGLFHKAIMESGVAIIPYL-EAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    546 TQLL 549
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                                                                                                                                                                                                                                                                                     --SEDCLYLNIYTBÁDLTKRDRLÞVMVWIHGGGLVLGGÁSTYDGLÁLSTHENVVVVVÍQY
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                                                                                                                                                                                                                                                                                                                                                                                LGŚLRPAPPOPAEPWSFVKNTTŚYPPWCSODPVAGQIVNDLLTNW----EENISLQF---
                                                                                                                                                                                                                                                                                                                                                                                                                              LGSLRFTNPQPASPWDNLREATSYPNLCLQN-----SEWLLLDQHMLKVHYPKF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ĊLYALILVFĹAAFTAĠ--ĠHPSSLĖVVDŤLQĠKVLĠKYŸSLEĠFTQĖŸAŸĖĹĠŸĖFĀĶĖĖ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CFFLILQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAPP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ĒĒIKLŠKOVNKFWANFĀRNGNPNARGLPHWPQYDOKĒBYLOIGATTQOSORLKAESVAFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRYDFW 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATE 485
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DKKMAIMLLEKFASIYGIPEDIIPVAIEKYRKGSDDPIKIRDGILAFIGDVLFCIPSVMV 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRDHRDAGAFTYVYEYQYYPSFSSPQRPKDVVGDHADDVYSVFGAPILR-----DGASE 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.5%; Score 1123; 42.2%; Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-May-1995 #text_change 09-Jul-2004
                                         -RVVDGAFFPNEPLDLLSQKAFKAIPSII 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; DB 2;
2.7e-80;
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A;Molecule type: protein
A;Residues: 19-26,'D',28-37 <GAU>
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum;
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-565/Product: carboxylesterase #status predicted <MAT>
F;50-551/Domain: cholinesterase homology <CHE>
F;79,489/Binding site: carbohydrate (Asn) (covalent) #status pr
                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-185,'0,'187-422,'M',424-505,'N',507-565 <MED>
A;Residues: 1-185,'0,'187-422,'M',424-505,'N',507-565 <MED>
A;Cross-references: EMBL:X65296; NID:g57553; PIDN:CAA46391.1; PID:g57554
B;Gaustad, R.; Sletten, K.; Lovhaug, D.; Fonnum, F.
Blochem, J. 274, 693-697, 1991
A;Title: Purification and characterization of carboxylesterases from rat
A;Reference number: S14361; MUID:91190080; PMID:2012599
                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 19-48 <MOR>
R;Medda, S:, Proia, R.L.
Bur. J. Biochem. 206, 801-806, 1992
A;Title: The carboxylesterase family exhibits C-terminal
A;Reference number: 823460; MUID:92299008; PMID:1606962
A;Accession: 823460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-264,'K', 266-565 <ROB2>
A;Cross-references: EMBL:X51974; NID:g56898; PIDN:CAA36236.1; PID:g56899
Arch. Blochem. Blophys. 315, 495-512, 1994
A;Title: Purification and Characterization of two rat liver microsomal conference number: S51202; MUID:95077430; PMID:7986098
                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-565 <ROB1>
A;Cross-references: UNIFROT:Q9R135; EMBL:X51974
A;Mote: 168-Gln. 247-Lys, 423-Met, and 506-Asn were also found
A;Note: the sequence from Fig. 4 is inconsistent with that from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N;Alternate names: hydrolase A
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: $10367; $12468; $51202; $23460; $14361
R;Robbi, M; Beaufay, H,; Octave, J.N.
Biochem. J. 269, 451-458, 1990
A;Fitle: Nucleotide sequence of cDNA coding for rat liver pI 6.1 esterase (1 A;Reterence number: $10367; MUID:90351366; PMID:2386485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, A;Reference number: S12468
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525
                                                                                                                                                                                                          352 QEFGWIIPTLMGYPLSEGKLDQKTAKSL-LMKSYPTLKISEKMIPVVAEKYFGGTDDPAK 410
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                                                                                                         471 FSVFGSPFLK-----DGASEEETNLSKMVMKYWANFARNGSPNGGGLPHWPEYDQKEGY 524
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                                                                                                                                     RFVFGGAFLKGDIVMFBGATEBEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTBQY 524
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LKIGASTQAAQRLKDKEVAFWSE----LRAKEAAEEP 557
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Search completed: June 16, 2005, 20:45:45 Job time : 45 secs

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## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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                                                            EMBL; BC069501; ANH69501.1; -.
HSSP; P12337; 1K4Y.
GO; GO:0003824; F:catalytic activity; IEA.
InterPro; IPR002018; CarbesteraseB.
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Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
FLJ31547 protein.
Name=FLJ31547;
Hydrolase.
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Director MGC Project;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Mammalia; Eutheria;
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A Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

A Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

A Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,

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A Murakami K., Yasuda T., Iwayanagi T., Mayatsuma M., Shiratori A.,

RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

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                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=FLJ31547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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Primates; (
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Pred. No. 6.2e-214;
3; Mismatches 6;
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RX MEDLINE=22388257; PubMede12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Hichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards N., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Butterfield Y.S.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 501
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Lisubmitted (APR-2004) to the EMBL/GenBank/DDBJ databases.

C -1 -SIMILARITY: Belongs to the type-B carboxylesterase/lipase fam.

REMBL; AKO56109; BAB71094.1; -.

REMBL; BC065948; AAH69548.1; -.

REMBL; BC069548; AAH69548.1; -.

REMBL; BC0605048; P:hydrolase activity; IEA.

REMBL; BC06016787; F:hydrolase activity; IEA.

REMBL; BC06016787; P:hydrolase activity; IEA.

REMBL; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060187; BC060
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RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Moniyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA RA Mishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzuni Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komateu T.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komateu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
"Complete sequencing and characterization of 21,243 full-length human
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TISSUE=PCR rescued
                                                                                                                                                                                                                                                                             501;
                                                                                      91
                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                    REATSYPNICLONSEWILLIDOHMIKVHYPKFGVSEDCLYLNIYAPAHADTGSKIPVLVWF
                                    REATSYPNLCLQNSEWLLLDQHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVWF
                                                                                                                                                                                                                                                                   84.6%;
ilarity 90.9%;
Conservative
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                                                                                                                                                                                                                                                         Score 2606; D
Pred. No. 2.2e
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                                                                                                                                                                                                                                                      DB 2;
2.2e-190;
les 0;
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RX PubMed=14702039; DOI=10.1038/ng1285;

RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

RA Wakamatsu A., Hayashi K., Sato H., Nagai S., Tanaka T., Ishii S.,

RA Wakamatsu A., Hayashi K., Sato H., Shibahara T., Tanaka T., Ishii S.,

RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,

RA Wakamatsu K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,

RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,

RA Makashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,

RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,

RA Ale K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yimoza M.,

RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,

RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,

RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,

RA Ono Y., Takajuchi S., Watanabe M., Takeuchi K., Arita M., Imose N.,

RA Masashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,

RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,

RA Moriya S., Komai F., Hara R., Takami S., Terashima Y., Suzuki O.,

RA Yoshikawa Y., Matanabe T., Sugiyama A., Takemoto M., Kawakami B.,

RA Yoshikawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

RA Hishigaki H., Watanabe T., Sugiyama A., Takuma S., Fukuzumi Y.,

RA Yamazaki M., Watanabe T., Kimagai A., Takuma S., Fukuzumi Y.,

RA Kawabata A., Hikiji T., Kobateke N., Inagaki H., Ikama Y., Okamoto S.,

RA Matesumura K., Makajima Y., Mizuno T., Morinaga M., Sasaki M.,

Matesumura K., Makajima Y., Mizuno T., Morinaga M., Sasaki M.,
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01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2003 (TrEMBLrel. 25,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens (Human).
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Best Local S
Matches 467
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InterPro; IPR0022018; CarbesteraseB.
InterPro; IPR000379; Ser_estrs.
Pfam; PR00135; COGETERASE; 1.
PROSITE; PS00122; CARBOXYLESTERASE_B_1;
PROSITE; PS00941; CARBOXYLESTERASE_B_2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Belongs to the EMBL; AK090997; BAC03565.1; -- HSSP; P12337; 1K4Y.
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                      LGQRLKEPRVDFWTSTIPLILSASDMLHSPLSSLTFLSLLQPFFFFFCAP
                                                                          LKGDIYMFEGATEEEKLLSRKWMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMS
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LGQRLKEPRVEFWTSTIPLILSASDMLHSPLSSLTFLSLLQPFFFFCAP
                                                           LKGDIVMFEGATEBEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMS
                                                                                                                                           LGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAF
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Pred. No. 7.
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Q6AW47 PRELIMINARY; PRT; 575 AA.
Q6AW47;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Carboxylesterase-like urinary excreted protein.
           SEQUENCE
Miyazaki
                                             NCBI_TaxID=9615;
                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                   Canis familiaris (Dog).
                                                                                              Name=cauxin;
CE FROM N.A.
ki M., Yamashita T
n family protein."
                                                           Chordata; C
  Taira
                                                           Craniata; Vertebrata; ; Fissipedia; Canidae;
             Ξ.
             Suzuki
                                                               Canis
                                                                         Euteleostomi;
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Best Local S
Matches 417
   SEQUENCE
Miyazaki
                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                            Q6AW46 PRELIMINARY; PRT; 575 AA.
Q6AW46;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Carboxylesterase-like urinary excreted protein.
Name=cauxin;
                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (AUG-2004) to the EMBL/GenBank/I
-!- SIMILARITY: Belongs to the type-B cark
EMBL; AB186392; BAD35015.1; -.
GO; GO:003824; F:Gatalytic activity; IEA.
InterPro; IPR00218; CarbesteraseB.
InterPro; IPR00219; Ser_estrs.
Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE_B_2; 1.
PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
Hydrolase.
SEQUENCE 575 AA; 63620 MW; 1005C35E82E
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 Yamashita
           z
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ilarity 75.7%;
Conservative 61
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Taira
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                               Craniata; Vert
Sciurognathi;
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the type-B carboxylesterase/lipase
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Pred. No. 4e-163;
1; Mismatches 73;
Ή,
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Suzuki
                             Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Mus
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                                   Q81034 PRELIMINARY; PRT; 545 AA.
Q81034;
Q81034;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Carboxylesterase-like urinary excreted protein.
                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                "cauxin family protein.";
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase
EMBL; ABL8639; BAD35016.1; -
GO:0003824; P:catalytic activity; IEA.
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000279; Ser estrs.
Pfam; PF00115; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE_B_2; 1.
PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase.
SEQUENCE
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390; Conserv
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                                                                                                       ILSASKALLSPTFSLILLSLLSPVLLSAA
                                                                                                                ILSASDMLHSPLSSLTFLSLLQPFFFFCA
                                                                                                                             KTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPMKEAPEILSGSNKS 371
                                                                                                                                                                                                                                575 AA;
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                                                                                                                                                                                                                                                                                                                                                                                           64166 MW;
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68.5%; Pred. No. 3e-151;
tive 69; Mismatches 9
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SEQUENCE

FROM N.A.

Pelis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; (Mammalia; Eutheria; Carnivora;
NCBI\_TaxID=9685;
[1]

Craniata; Vertebrata; ; Fissipedia; Felidae;

Euteleostomi; Felis.

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RESULT 7
Q95KH3
ID Q95K
AC Q95K
DT 01-D
DT 01-D
DT 01-C
DT 01-C
DT 01-C
C MACA
OC MACA
OC MACA
OC MACA
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Best Local
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SEQUENCE
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EMBL; AB045377; BAC22577.1; -.

HSSP; P123377; IK4Y.

GO; GO:0016787; F:hydrolase activity; IEA.

InterPro; IPR002018; CarbesteraseB.

InterPro; IPR002018; CarbesteraseB.

InterPro; IPR0020379; Series

Pfam; PF00135; COesterase; 1.

PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.

PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.
                                                                                                                                                                                                             Q95KH3; PRELIMINARY;
Q95KH3; O1-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22458314; PubMed=12401131; DOI=10.1042/BJ20021446; Miyazaki M., Kamile K., Soeta S., Taira H., Yamashita T.; Molecular cloning and characterization of a novel carboxylesterase-like protein that is physiologically present at high concentrations the urine of domestic cats (Felis catus)."; Biochem. J. 370:101-110(2003).
Hypothetical protein.

Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Macaca.

NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Kidney;
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TISSUE=Uropygial gland;

WEDLINE=93300823; PubMed=8314791;

Hwang C.-S., Kolattukudy P.E.;

Hwang C.-S., Kolattukudy P.E.;

Hwang C.-S., Kolattukudy P.E.;

Hwang C.-S., Kolattukudy P.E.;

Hwang C.-S., Kolattukudy P.E.;

Hwang C.-S., Kolattukudy P.E.;

Hwang C.-S., Kolattukudy P.E.;

Hwang C.-S., Kolattukudy P.E.;

Hwang C.-S., Kolattukudy P.E.;

Holl C.-S., Kolattukudy P.E.;

J. Biol Chem. 268:14278-14284(1993).

J. Biol. Chem. 268:14278-14284(1993).

J. Biol. Chem. 268:14278-14284(1993).

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J. Biol. Chem. 268:14278-14284(1993).

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J. Biol. Chem. 268:14278-14284(1993).

J. Fiol. Chem. 268:14278-14284(1993).

J. Biol. Chem. 268:14284(1993).

J. Biol. Chem.

in liver and kidney.
SIMILARITY: Belongs to the type-B

carboxylesterase/lipase

family.

Anas platyrhynchos (Domestic duck). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; Neognathae; Anseriformes; Anatida

Euteleostomi; Anas.

Aves; Neognathae; Anseriformes; Anatidae;

(Thioesterase B).

SEQUENCE FROM N.A., NCBI\_TaxID=8839;

AND SEQUENCE

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SEQUENCE FROM N.A.
TISSUE-Temporal lobe right;
TISSUE-Temporal lobe right;
Tanuma R.,
Tanuma R.,
Tanuma R.,
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Suzuki Y., Sugano S., Hashimoto K.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases:
-I- SIMILARITY: Belongs to the type-B carboxylesterase/lipase
EMBL, AB060873; BAB46884.1; -
HSSP, P12337; 1K4Y.
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01-FEB-1995 (Rel. 31,
25-OCT-2004 (Rel. 45,
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95.0%;
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SEQUENCE
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SIGNAL
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PIR; A47162; A47162
HSSP; O77540; IM4Y
InterPro; IPR0002018; CarbesteraseB.
InterPro; IPR000379; Ser_estrs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst. the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/ancor send an email to license@isb-sib.ch).
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RRRKHTDL
                     SDMLHSPL 563
                                                    KYWATFARTGNENGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIFLILSA
                                KYWTNFARNGNPNGEGLVHWPQYDMDERYLEIDLTQKAAKKLKERKMEFWMQLTEQIMSD
                                                                                    VYFYEFOHRPSSAAGVVPEFV
                                                                                         LALSFKGAPSDIVDĹVYNĖYIGVAENRAQVRDGĹĹĎSIADPLĖVFSAVEVARHHRĎAGNP
                                                                                                                                             LHI-----POYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAP
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                                                                                                                                                                                          GAPFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLP-MKEAPEILSGSNKSLALHLIQNI 380
                                                                                                                                                                                                                 LFTE----QPEEQAQRIAAAAGCEKSSSAALVECLREKTEAEMEQITLKMPPMFISASLD
                                                                                                                                                                                                                               QVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSBMAKGLFHKAIMESGVAI-I
                                                                                                                                                                                                                                                              ÓVAÁLQWIQENÍIHFRGDÞGSVTÍFGESÁGGVSVSALVLSÞLÁKGLFHKÁÍSESGTÁVRÍ
                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                     VRDÁASÝPPMČLODK---VĽGOYLSDAITNRKEKVRLOIŚEĎĆĽÝLNVYTÝVSTEEQEKĽ
                                                                                                                                                                                                                                                                                                                                                                      TGQKAEQPEVVTNYGSVRGYQVKVNAAERSVNVFLGLPFAKPPVGPLRFSBPQPPBPWKG
                                                                                                                                                                                                                                                                                                                                                                                                                     TGPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAPPLGSLRFTNPQPASPWDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS0012; CARBOXYLESTERASE B 1; 1.
PS00941; CARBOXYLESTERASE B 2; 1.
PS00941; CARBOXYLESTERASE B 2; 1.
rotein sequencing; Fatty acid biosynthesis; Hydrolase; Signal.
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557 AA;
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476
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48.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1298.5;
Pred. No. 1.9e-
79; Mismatches
                                                                             VKADHADETAFVFGKPFLAGN----ATEEEAKLSRTVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acyl-ester intermediate (By similarii (Charge relay system (By similarity). Charge relay system (By similarity). By similarity.

N-linked (GlcNAc. . .) (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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RESULT 9

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091WG0
091WG0
01-DEC-2001 (TYEMBLYE1, 19, Created)
DT 01-DEC-2001 (TYEMBLYE1, 19, Created)
DT 01-DEC-2001 (TYEMBLYE1, 19, Created)
DT 01-DEC-2001 (TYEMBLYE1, 19, Created)
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X MEDLINE=274405; PubMed=12859986; DOI=10.1016/S0003-9861(03)00286-8; A Furihata T., Hosokawa M., Nakata F., Satoh T., Chiba K.; T "Purification, molecular cloning, and functional expression of inducible mouse liver acylcarnitine hydrolase in C57BL/6 mouse, arch. Biochem. Biophys. 416:101-109(2003).

Arch. Biochem. Biophys. 416:101-109(2003).

C -- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family. RMBL; BC015290; AAH15290.1; --

REMBL; BC034159; AAH24552.1; --

DR EMBL; BC034170; AAH31170.1; --

DR EMBL; BC034191; AAH34178.1; --

DR EMBL; BC034191; AAH31180.1; --

DR EMBL; BC034191; AAH3180.1; --

DR EMBL; BC034191; AAH3180.1; --

DR EMBL; AB110073; BAC76623.1; --

DR EMBL; AB110073; BAC76623.1; --
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RA Klausner R.D., Collins F.S., Wagner L., Schamen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Sunfard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J.. Marra M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Generation and initial analysis of more than 15,000 and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Sciurognathi;
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rase ML3 precursor)
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thi; Muridae; Murinae; Mus
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Best Local S
Matches 276
                                               Ol-MAR-2003 (TrEMBIrel. 23, Created)
01-MAR-2003 (TrEMBIrel. 23, Last sequence update)
05-UUL-2004 (TrEMBIrel. 27, Last annotation update)
05-UUL-2004 (TrEMBIrel. 27, Last annotation update)
Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
RIKEN full-length enriched library, clone:5031415B19 product:similar
to CARBOXYLESTERASE (EC 3.1.1.1) (ALI-ESTERASE) (B-ESTERASE)
(MONOBUTYRASE) (COCAINE ESTERASE) (PROCAINE ESTERASE) (METHYLBUTYRASE)
(9030624L02Rik protein).
                                                                                                                                   Q8BK48;
Q8BK48;
01-MAR-2003
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SEQUENCE
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GO:0005615; C:extracellular space; 7

GO:0005015; Coesterase; 1.

PROSITE; PS00122; CARBOXYLESTERASE B 1;

PROSITE; PS00941; CARBOXYLESTERASE B 2;
 Eukaryota; Metazo
Mammalia; Eutheri
NCBI_TaxID=10090;
                                    Name=9030624L02Rik;
Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPHKAIMESGVAIIPYLEAHDYEKSEDLQ-VVAHFCGNNASDSEALLRCLRTKPSKELLT
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                                                                                                                                                                                                                                       LKAGRLQFWTKTLPQKIQELKASQDKHREL
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                                                                                                                                                                                                                                                                                                              IVMFEGATEEEKLISRKWMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQR
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           Eutheria;
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              Chordata;
Rodentia;
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            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                         (METHYLBUTYRASE)
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SEQUENCE FROM N.A.

C STRAIN-C578L/61, TISSUE-Ovary and uterus;

Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

Adachi J., Aizawa K., Akimura T., Arakawa T., Hashizume W.,

Alayashida K., Furuno M., Hanagaki T., Hara A., Hashizume T.,

Alayashida K., Hayatsu N., Hiramoto K., Hiraoka T.,

Alayashida K., Hayatsu N., Ishi Y., Itoh M., Kagawa I., Kasukawa T.,

Akatoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

Kurihara C., Mateuyama T., Miyazaki A., Murata M., Nakamura M.,

Akatoh H., Kawai J., Wumazaki R., Ohno M., Ohsato N., Okazaki Y.,

Aka Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

Aka Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

Tagawa A., Takahashi F., Takakaku-Akahira S., Takeda Y., Tanaka T.,

An Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP SEQUENCE FROM N.A.

(C STRAIN=C57BL/6J; FISUE=Ovary and uterus;

(C STRAIN=C57BL/6J; PubMed=11076861; DOI=10.1101/gr.152600;

(MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

(A) Suni N., Ishii Y., Nakamura K., Nagaoka S., Sasaki N., Carninci P.,

(A) Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

(A) A Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Kashiwagi K.,

(A) A Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

(A) Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

(A) Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

(A) Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

(A) Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

(A) Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

(B) Genome Res. 10:1757-1771(2000).
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SETRAIN=FVB/N; TISSUB=Colon;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22382257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22382257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22382260389;

MEDLINE=223822603899;

MEDLINE=223822603899;

MEDLINE=223822603899;

MEDLINE=243822603899;

MEDLINE=24382
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Ovary and u
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM Consortium;
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Nature 420:563-573(2002).
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SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Ovary and uterus;
MEDLINE=99279253; PubMed=10349636; DOI=10
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STRAIN=C57BL/6J; 1
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STRAIN=C57BL/6J; TISSUE=Ovary
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; DOI=10.1038/35055500
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Best Local Sim:
Matches 260;
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A Straubberg R.;

L Submitted (VIII-2003) to the EMBL/GenBank/DDBJ databases.

C -1-SIMILARITY: Belongs to the type-B carboxylesterase/lipa

R EMBL; AK077248; BAC35707.1; -.

R EMBL; BC055062; AAH55062.1; -.

R HSSP; p12337; 1K4Y.

R MGD; MGI:2443170; 9030624102Rik.

R GO; GO:0005615; C:extracellular space; TAS.

InterPro; IPR002018; CarbesteraseB.

InterPro; IPR00379; Ser estre.

DR InterPro; IPR003379; Ser estre.

DR PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.

DR PROSITE; PS00121; CARBOXYLESTERASE B 2; 1.

DR PROSITE; PS00121; CARBOXYLESTERASE B 2; 1.
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SEQUENCE
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STRAIN=FVB/N; TISSUE=Colon;
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                                          YWANFARHGNPNSEGLPYWPVMDHDEQYLQLDIQPSVGRALKARRLQFWTKTLP
                                                                     YWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIP
                                                                                                  YFYEFQHRÞSFFKDFRÞPYVKADHGDEIFLVFGYQF--GNÍKL--PYTEEEEQLSRRIMK
                                                                                                                      YFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRXMK
                                                                                                                                                              M-----LÞÞECGDĹLMEÈYNGDTEDPETLQAQFREMKĠĎFMFŸIÞÁLQVÁHFQŔ-SHÁÞÝ
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48.7%; Pred. No. 4.2e-89;
tive 79; Mismatches 165;
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Best Local Sim
Matches 262;
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SEQUENCE FROM N.A.
STRAIN=Syrian golden; TISSUE=Liver;
Sone T., Wang C.Y.,
"Microsomal amidases and carboxylesterases.";
(In) Guengerich F.P. (eds.);
COMPREHENSIVE TOXICOLOGY VOLUME 3, Biotransformation,
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Syrian golden; TISSUE-Liver;
Sone T., Ishida Y., Takabatake E., Wang C., Isobe M.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase
EMBL; D50577; BAA23605.1; --
HSSP; P12337; 1K4Y.
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PRELIMINARY; PRT; 559 AA.
O35533;
O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Carboxylesterase precursor (EC 3.1.1.1).
Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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NCBI_TaxID=10036;
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HRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKVMKYWATFA
                         LPPECGDLLMEEYMGDNEDPQTLQAQFREMMGDFTFVIPSLQVAHFQR-
                                        IPPOYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEFR
                                                                        KHPQELLASADFDPVPSIIGVNNDEYGWLVPVIMGSAQEIKEITRVTLPAILKSTANQMK
                                                                                              NEPLDILSOKAFKAIPSIIGVNNHECGFILP--MKEAPEILSGSNKSL--ALHLIQNILH
                                                                                                                         ISSSEMV--YTIVANLSDCAAVNTETLVSCLRGKSEAEILAINKVFKIIPAVVDGEFLP
                                                                                                                                                                                                                                          LVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQV
                                                                                                                                         EAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFP
                                                                                                                                                                           AALRWVQQNIAHFGGNFGQVTIFGESAGGTSVSSHVVSFNSKGLFHGAINESGVSVMFGI
                                                                                                                                                                                        AALSWVQKNIEFFGGDDSSVTIFGESAGAISVSSLILSDMAKGLFHKAIMESGVAIIPYL
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Pred. No. 9.2e-
79; Mismatches
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                                                                                                       SEQUENCE FROM N.A.

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STRAIN-C57BL/6J; TISSUE-Colon;
MEDLINE-20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs t
prepare full-length cDNA libraries for rapid discovery of new
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=Colon;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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01-MAR-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male colon cDNA, RIKEN full-length enriched library, clone:9030624L02 product:similar to CARBOXYLESTERASE (D-SCTERASE) (MONOBUTYRASE) (COCAINE ESTERASE) (METHYLBUTYRASE).
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SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Colon;
Aizawa K., Akimura T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUE=Colon;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the RIKEN Genome Exploration Research Group Phase I & II "Analysis of the mouse transcriptome based on functional 60,770 full-length cDNAs."; Nature 420:563-573(2002).
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RESULT Q6PDB7 ID Q6 AC Q6 DT 0: DT 0: DT 0: DT H

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(TrEMBLrel. 27, Created)
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A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
A Nishi K., Nomura K., Numazaki K., Sakato N., Okazaki Y.,
A Saitor R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Saitor R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR EMBL, AKO33563; BAC28361.1; -.
DR HSSP; P12337; 1K4Y.
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Best Local (
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PROSITE; PS00941; CARBOXYLESTERASE B 2;
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InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000379; Ser_estrs.
Pfam; PF00135; COesterase; 1.
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YRANFARHGNPNSEGLPYWPVMDHDEQYLQLDIQPSVGRALKARRLQFWTKTLP
                                  YWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIP 550
                                                                    YFYEFOHRPSFFKDFRPPYVKADHGDEIFLVFGYQF--GNIKL--PYTEEEEQLSRRMK
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  space;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
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                                                                                                                                                                                                              379
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                                                                                                         496
                                                                                                                                         433
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Query Match
Best Local Sim
Matches 273;
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RC STRAIN=SVB/N, TISSUE=Colon;

RX MEDLINE=2238857; PubMeda12477932; DOI=10.1073/pnas.242603899;

RA Klausner R.D. Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Wollan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences ";

RI "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.
PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
-1-SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
EMBL; BC058815; AAH58815.1; -.
HSSP; P12337; 1K4Y.
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000379; Ser_estrs.
Pfam; PF00135; COesterase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=FVB/N; TISSUE=Colon;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                  172
                                                                                                                                                                                                                                                               112
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RGKSEAÉILAINKLVQMIPAVVDGEFFPRHPKELLASEDFHPVPŠÍÍGVNNDEFGWTIP-
                   RTKPSKELLTLSQKTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPM
                                                                           ŚŚHVVŚPMSKĠĹPHGAIMEŚĠVALLPYĹITDTSEMVS--TTVAKLSGCEAMDSEALVRCL
                                                                                                  SSLILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCL
                                                                                                                                                                                Similarity
                                                                                                                                                      I QYRLGVLGFFSTGDQHARGNWGFLDQVAALRWIQQNIAHFGGKFDRVT1FGBSAGGTSV
                                                                                                                                                                                                                                     PPVSTŠEDCLÝLNÍ ÝTPAHAHEGŠNÍ PVMÝMI HGGGLVAGMÁŠNYDGŠLÍ LÁALEDLVÝVT
                                                                                                                                                                                                                                                                        PKFGVSEDCLYLNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVV
                                                                                                                                                                                                                                                                                                                     GVHTFLGIPFAKPPVGPLRFAPPBAPBPWSGVRDGTAHPAMCLQN----LGVMKEIKLKL
                                                                                                                                                                                                                                                                                                                                                         PVNVFLGVPFAAPPLGSLRFTNPQPASPWDNLREATSVPNLCLQNSEWLLLDQHMLKVHY
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPQGLTSSASQWCFFLI---LQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical 556 AA; 619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                -SQMHNWLDVLLFGLLLLLGHVQ-GQDSPEA-SPIRNTHTGQVRGSLVHVKDTKA
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61927 MW; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1266.5; DB Pred. No. 5.3e-88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190;

 Length 556;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                           289
                                                                                                                 298
                                                                                                                                                        231
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buedow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulphy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulphy S.J.,
RA Rahey J., Helton E., Ketteman M., Madan A., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodriques S., Sanchez A.,
RA Rahiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriquez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences ";
RL Proc. Natl Acad. Sci. U.S.A. 99:16899-16893(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q6GN54;
Q6GN54;
Q5-JUL-2004 (TrEMBLrel. 27, Createq;
05-JUL-2004 (TrEMBLrel. 27, Last sequence update;
05-JUL-2004 (TrEMBLrel. 27, Last sequence update;
05-JUL-2004 (TrEMBLrel. 27, Last annotation upd;
E LOC443703 protein (Fragment).
Name=LOC443703; African clawed frog).
SXenopus laevis (African clawed frog).
SXenopus laevis (Chordata; Craniata; Vertek;
Privarvota; Metazoa; Chordata; Craniata; Vertek;
Name=LOC43703; Anura; Mesobatrachia; Pij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
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Klein S., Gerhard D.S.;
submitted (JUN-2004) to the EMBL/GenBa
-!- SIMILARITY: Belongs to the type-B
EMBL; BC074230; AAH74230.1; -.
GO; GO:0016787; F:hydrolase activity;
                                                                                                                                                                TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174; Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifto
                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                          wenetic and initiative.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                            225:384-391 (2002) .
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                                                                                                                                                                                                                                                                                                                                genomic
                                                                                                                                                                                                     N.A.
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                                                                                     EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                  Xenopus
                                               carboxylesterase/lipase
                                                                                                                                                                                                                                                                                                           research: The
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ia; Pipoidea; Pipidae;
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ion update)
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                                                                                                                                                                                                                                                                                                 NIH Xenopus
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RESULT 15
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Best Local S
Matches 258
                                                                                                                                                                                                                                                                                                                     O70177 PRELIMINARY;
O70177;
01-AUG-1998 (TrEMBLrel. 07, C:
01-AUG-1998 (TrEMBLrel. 07, L:
01-MAR-2004 (TrEMBLrel. 26, L:
Carboxylesterase precursor (E)
Name=carboxylesterase;
SEQUENCE FROM N.A.

STRAIN-Wistar; TISSUE-Small intestine;
Sone T., Kunitomo T., Isobe M.;
Sone T., Kunitomo T., Isobe M.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: Belongs to the type-B carboxylesterase/lipase EMBL; ABO10632; BAA55691.1; -.
HSSP; B37967; 1QE3.
G0; GO:0004091; F:carboxylesterase activity; IEA.
G0; GO:0016787; F:hydrolase activity; IEA.
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PROSITE; PS
Hydrolase.
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InterPro; IPR000379; Ser estrs.
Pfam; PF00135; Coesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE_B_1;
PROSITE; PS00941; CARBOXYLESTERASE_B_2;
                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LMA---SKTEKILPILHVVANISSCSVSSLADCLKKKTEDEIVAISAAMKFVAFPAVVDG
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Pred. No. 9.2e-88;
7; Mismatches 169; Indels
                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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InterPro; IPR000379; Ser_estrs.
Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE_B_1;
PROSITE; PS0991; CARBOXYLESTERASE_B_2;
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                                                              VFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQ
                                                                                                             DSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRF
                                                                                                                                                  TIPMVMGTAQIIKE----LSRENLQAVLKDTAAQMMLPPECGDLLMEEYMGNTDDSQTLQ
                                                                                                                                                                         LLPM-----KEAPEILSGSNKSLALHLIQNILHIPPQYLHLVANEYFHDKHSLTEIR
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LDTHPAVDRALKARRLQFWTKTLP
                    LDLNMSLGQRLKEPRVDFWTSTIP 550
                                                 VF-GSFFSGMKLDF---TEEERLLSRRMMKYWANFARQGNPNSEGLPYWPALDHDEQYLQ
                                                                                               IQYTEMMGDELFVIPALQVAHFQR-SHAPVYEYEFQHAPSYFKNVRPPHVKADHADEVPF
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561 ca
62239 MW;
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48.8%; Pred. No. 1.1e-87;
vative 77; Mismatches 179
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; Patent No. 6664091
; GENERAL INFORMATION:
   APPLICANT: Curtis, Rory A. J.
   APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-122001
; CURRENT APPLICATION NUMBER: US/10/023,515
; CURRENT APPLICATION NUMBER: 00/256,369
; PRIOR APPLICATION NUMBER: 60/256,369
; PRIOR FILING DATE: 2001-12-18
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NOS: 6
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; TYPE: PRT
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Sequence 28, Application US/09595682B

Patent No. 6800483

GENERAL INFORMATION:
APPLICANT: Danks, Mary K.
APPLICANT: Potter, Philip M.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of TITLE OF INVENTION: Tumor Cells

CURRENT APPLICATION NUMBER: US/09/595,682B

CURRENT FILING DATE: 2000-01-16

PRIOR FILING DATE: 1998-02-19

PRIOR PILING DATE: 1998-02-19

PRIOR APPLICATION NUMBER: PCT/US99/03171

PRIOR FILING DATE: 1999-02-12

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin Ver. 2.0

LENGTH: SS9

LENGTH: SS9
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                      FFPNEPLDLLSGKAFKAIPSIIGVNWHECGFLLP----MKEAPEILSGSNKSLALHLIQN
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                                  LIA----SŚADVISTVVANLSACDQVDŚEALVGCLRGKSKEEILAINKPFKMIPGVVDGV
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PRICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
SOFTWARE: FASTSEQ for Windows Version 4.
SEQ ID NO 6426
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; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6426
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US-09-949-016-6426
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Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
              437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 GESAEGPORNIKLGWIOCKOVIVLGSPVPVNVELGVPFAAPPLGSLKFINPOPASPWDNL 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 39.9%; Score 1230; DB 4; Similarity 46.7%; Pred. No. 4.8e-125; 48; Conservative 91; Mismatches 168;
EFQHQPSWLKNIRPPHMKADHGDELPFVF-RSFFGGNYIKF---TEEEEQLSRKNNKYWA
                              EFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKWMKYWA
                                                                 LEAHDYEKSEDL--QVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGA 323
                                                                                                                                                                                                                                                                                          VAALSWVQKNIEEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIPY 265
                                                                                               I HI PPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFY
                                                                                                                                FLPRHPQELLASADFQPVPSIVGVNNNEFGWLIPKVMRIYDTQKEMDREASQAALQKMLT 377
                                                                                                                                                    FFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLP----MKEAPEILSGSNKSLALHLIQN 379
                                                                                                                                                                                                     LIA----SŚADVISTVVANLSACDQVDŚEALVGCLRGKSKEEILAINKPFKMIPGVVDGV
                                                                                                                                                                                                                                                                        VAALRWVQQNIAHFGGNPDRVTIFGESAGGTSVSSLVVSPISQGLFHGAIMESGVALLPG
                                                                                                                                                                                                                                                                                                                                           REATSYPNICION-----SEWILLDQHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GQDSASÞÍRTTHTGQVLGSLVHVKGANAGVQTFLGIÐFAKÞÐLGÐLRFAÞÐEÐÐESWSGV 85
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CLOOL307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-3
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
VUMBER OF SEQ ID NOS: 207012
SOFTMARE: FASCSEQ for Windows Version 4.0
SEQ ID NO 9670
LENGTH: 577
TYPE: PT
ORGANISM: Human
US-09-949-016-9670
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Best Local S
Matches 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQ 205
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NFARNGNPNGEGLPHWPLFDQEEQYLQLNLQPAVGRALKAHRLQFWKKALP 561
                                                                                                                                                               LLMLPPTFGDLLREEYIGDNGDPQTLQAQFQEMMADSMFVIPALQVAHF-QCSRAFVYFY
                                                                                                                                                                                                                                                                       FFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLP----MKEAPEILSGSNKSLALHLIQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REATSYPHICLON----SEWILLDQHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLP 145
                                                                                                                      EFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWA 499
                                                                                                                                                                                                   ILHIPPOYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFY
                                                                                                                                                                                                                                                                                                                              LIA----SSADVISTVVANLSACDQVDSEALVGCLRGKSKEEILAINKPFKMIPGVVDGV
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                                      TFARTGUPNGUDLSLWPAYULTEQYLQLDLUMSLGQRLKEPRVDFWTSTIP 550
                                                                                EFQHQPSWLKNIRPPHMKADHGDELPFVF-RSFFGGNYIKF---TEEBEQLSRKMMKYWA
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RESULT 5 US-09-595-682B-21

RESULT 6
US-09-264-737-2
; Sequence 2, Application US/09264737A
; Patent No. 6107549

GENERAL INFORMATION:

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APPLICANT: Danks, Mary K.

APPLICANT: Potter, Philip M.

APPLICANT: Houghton, Peter J.

ITILE OF INVENTION: Compositions and Methods

TITLE OF INVENTION: Tumor Cells

FILE REFERENCE: SJ-0005

FILE REFERENCE: SJ-0005

CURRENT APPLICATION NUMBER: US/09/595,682B

CURRENT FILING DATE: 2000-01-16

PRIOR APPLICATION NUMBER: 60/075,258

PRIOR APPLICATION NUMBER: PCT/US99/03171

PRIOR APPLICATION NUMBER: PCT/US99/03171

PRIOR FILING DATE: 1999-02-12

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIFGFFTTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLIL 243
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                           SLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWT 546
                                                                                                                                                                                                                                                                                                                                                                              SEDCLYLNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLGSLRPAPPQPAESWSHVKNTTSYPPMCSQDA----VSGHMLSELFTNRKENIPLKF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHML-----KVHYP-KFGV 123
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POWPAYDYKEGYLQIGATTQAAQKLKDKEVAFWT
                                                                        PKTVIGDHGDEIFSVLGAPFLK-----EGATEEEIKLSKMVMKYWANFARNGNPNGEGL
                                                                                            PAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWATFARTGNPNGNDL 512
                                                                                                                                                   EKYLGGTDDPVKKKDLFLDMLADLLFGVPSVNVARHHRDAGAPTYMYEYRYRPSFSSDMR
                                                                                                                                                                                                                          inqqefgwiipmqmlgyplsegkldqktatellwks---
                                                                                                                                                                                                                                                             VNNHECGFLLPM------KEAPEILSGSNKSLALHLIQNILHIPPQYLHLVA 392
                                                                                                                                                                                                                                                                                                                                                                                                                   SPMAKGLFHKAIMESGVAIIPYLEAHDYEKSED--LQVVAHFCGNNASDSEALLRCLRTK 301
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Sequence 26, Application US/0959568;
Patent No. 6800483
GENERAL INFORMATION:
APPLICANT: Danks, Mary K.
APPLICANT: Potter, Philip M.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions ar
TITLE OF INVENTION: Tumor Cells
FILE REFERENCE: SJ-0005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Feng, Paul C.C.

APPLICANT: Ruff, Thomas G.

ITITLE OF INVENTION: Engineering Plant Resistance to Pyridines via
ITITLE OF INVENTION: Expression of Esterase Enzymes

FILE REFERENCE: 38-21(10551) RLE3 Pyridine Tolerance

CURRENT APPLICATION NUMBER: US/09/264,737A

CURRENT FILING DATE: 1999-03-09

FARLIER APPLICATION NUMBER: 60/077,377

EARLIER APPLICATION NUMBER: 50/077,377

IEARLIER FILING DATE: 1988-03-10

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin Ver. 2.0

LENGTH: 566

TYPE: PRT

ORGANISM: Rabbit
US-09-264-737-2
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Best Local :
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                                                                                                                                                                                            POWPAYDYKEGYLÓIGATTQAAÓKLKDKEVAFWT
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43.6%;
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Pred. No. 5.1e-115;
5; Mismatches 176;
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                    Methods for Sensitizing
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Sequence 2, Application Patent No. 5817490

US/08845295A

GENERAL

INFORMATION:

APPLICANT: Hubbs, Jo TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:

VENTION: Enzymatic Process for the Manufacture VVENTION: Enzymatic Process for the Manufacture VVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, VVENTION: 2-Keto-L-Gulonic Acid

Esters

of.

NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:

ADDRESSEE: STREET: P. CITY: King

Kingsport

E: Eastman C P.O. Box 511

Chemical

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US-09-595-682B-26
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Best Local S
Matches 249
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249; Conserv
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                                                POWPAYDYKEGYLOIGATTQAAQKLKDKEV
                                                                          SLWPAYNLTEQYLOLDLNMSLGQRLKEPRV
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                                                                                                                          PAFYKADHADEVRFYFGGAFLKGDIVMFEGATEEEKLLSRKWMKYWATFARTGNPNGNDL
                                                                                                                                                      EKYLGGTDDPVKKKDLFLDMLADLLFGVPSVNVARHHRDAGAPTYMYEYRYRPSFSSDMR
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COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch disk

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TELEPHONE: 423-229-6189
TELEFAX: 423-229-1239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Windows SOFTWARE: Microsoft Word CURRENT APPLICATION DATA:
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les 259; Conserv
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REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 25-April-97 CLASSIFICATION: 435
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NFARSGNPNGEGLPHWPFTMYDQEEGYLQIGVNTQAAKRLKGEEVAFWNDLL 568
                                   TFARTGNPNGNDLSLWP--AYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTI 549
                                                                                                                                                                                                 YLHLVANEYFHDKH-----SLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEF 441
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                                                                             QYRPSFSSDKFTKPKTVIGDHGDEIFSVFGFPLLKGD----APEEEVSLSKTVMKFWA
                                                                                                                 RHRPQCFED--TKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATESEKLLSRKMMKYWA 499
                                                                                                                                                                                                                                         TVPYIVGINKQEFGWLLPTMMGFPLSEGKLDQKTATSLLWKS-----YPIANI----PE
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PACENT NO. 6022719
GENERAL INFORMATION:
APPLICANT: Hubbs, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 423-229-6189
TELEFAX: 423-229-1239
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017
APPLICATION NUMBER: 17-May-96; 25-Ap
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 7043
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: Windows 95
SOPTWARE: MicroBoft Word
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 584 amino TYPE: Amino Acid TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Kingsport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 35.4%; Score 1091.5; DB 3 Local Similarity 43.8%; Pred. No. 7.4e-110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                              70 APPLGSLRFTNPQPASPWDNLREATSYPNLCLQNS--EWLLLD-----QHMLKVHYPK 120
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                               CLRTKPSKELLTLSQKTKSFT-------RVVDGAFFPNEPLDLLSQK--AFK 339
                                                                                                     SVSSLILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLR
                                                                                                                                                                         VQYRLGIFGFFTTWDQHAPGNWAFKDQVAALSWVQKNIBFFGGDDSSVTIFGES--AGAI
                                                                                                                                                                                                                                                                  FGVSEDCLYLNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYED--VLVVV 178
                                                                                                                                                                                                                                                                                                        KPPLGSLRFAPPQPAEPWSFVKNTTSYPPMCCQDPVVEQMTSDLFTNFTGKERLTLEF--
                                                                                                                                                                                                                                                                                                                                                                                  WLLPLVLTSLASSATW--AGOPASPPVVDTAQGRVLGKYVSLEGLAFTQPVAVFLGVPFA
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CLRQKSEDELLDLTLKMKFUTLDFHGDQRESHPFLPTVVDGVLLPKMPEEILAEKDFTFN
                                                                           SVSVLVLSPLAKNLFHRAISESGVALTVALVRKDMKAAAKQIAVLAGCKTTTSAVFTFVH
                                                                                                                                                     I QYRLGIWGFFSTGDEHSRGNWGHLDQVAALHWVQENIANFGGDPGSVTIFGESFTAGGE
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P.O. Box 511
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                                                                                                                                                                                                                                SEDCLYLNIYTPADLTKRGRLPVMVWIHGGGLVLGGAPMYDGVVLAAHENFTVVVVA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               63; Mismatches 191;
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; MOLECULE TYPE:
US-09-146-661-2
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US-09-146-661-2
                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
FILING DATE: 17-May-96; 25
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,34
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                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 70.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: MICTOSOFT WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144
FILING DATE: 03-Septmeber-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
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TITLE OF INVENTION:
TITLE OF INVENTION:
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CITY: Kingsport
STATE: Tennessee
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                    LENGTH: 584 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
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                                                                                                         12 WCFFLILQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTV--LGSPVPVNVFLGVPFA 69
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                                         APPLGSLRFTNPQPASPWDNLREATSYPNLCLQNS--EWLLLD------QHMLKVHYPK 120
        KPPLGSLRFAPPOPAEPWSFVKNTTSYPPMCCODPVVEOMTSDLFTNFTGKERLTLEF--
                                                                           WLLPLVLTSLASSATW--AGQPÁSPÞVVDTAQGRVLGKYVSLEGLAFTQÞVAVFLGVÞFÁ
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                                                                                                                                                                                                                                                           Linear
                                                                                                                                                                                                                                                                                                                                                        423-229-6189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enzymatic Process for the Manufacture of Ascorbic Acid, 2-Keto-L-Gulonic Acid, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chemical Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US 60/017,879; 08/845,295
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                                                                                                                                                  63;
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                                                                                                                                                                                                                                                                                                                                                                                          70432
                                                                                                                                                  Mismatches
                                                                                                                                                191;
                                                                                                                                              Indels
                                                                                                                                                                               Length
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PRINTERAL INFORMATION:
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US-09-150-515-2
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                                                            FILING DATE: 17-MAY-96; 25-April-97
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 70432
TELECOMMUNICATION INFORMATION:
TELEPHONE: 423-229-6189
                                 TELEFAX: 423-229-1239 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                   ZIP: 37662-5075
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch d
COMPUTER: IBM Compatibl
OPERATING SYSTEM: Windo
     SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acid
                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                   SOFTWARE: Microsoft Word CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eastman Chemical Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hubbs, John C.
TITLE OF INVENTION: Enzym
TITLE OF INVENTION: Ascor
TITLE OF INVENTION: 2-Ket
                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 09-SE
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CITY: Kingsport
STATE: Tennessee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       340 AIPSIIGVNNHECGFLLP-------WKEAPEILSGSNKSLALHLIQNILHIPPQ 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09150515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NFARSGNPNGEGLPHWPFTMYDQEEGYLQIGVNTQAAKRLKGEEVAFWNDLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELTPVAT--FTDKYLGGTDDPVKKKDLFLDLMGDVVFGVPSVTVARQHRDAGAPTYMYEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLRTKPSKELLTLSQKTKSFT--------RVVDGAFFPNEPLDLLSQK--AFK 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLRQKSEDELLDLTLKMKFLTLDFHGDQRESHPFLPTVVDGVLLPKMPEEILAEKDFTFN 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---ŚEDCLYLNIYTPADLTKRGRLPVMVWIHGGGLVLGGAPMYDGVVLAAHENPTVVVVA
584 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                            P.O. Box 511
                                                                                                                                                                                                                                                                                                    IBM Compatible
SYSTEM: Windows
                                                                                                                                                                                                                                        09-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enzymatic Process for the Manufacture Ascorbic Acid, 2-Keto-L-Gulonic Acid, 2-Keto-L-Gulonic Acid
                                                                                                                                                                               US 60/017,879; 08/845,295
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; TYPE: Amino Acid
; TOPOLOGY: Linear
; MOLECULE TYPE: protein
US-09-150-515-2
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                                         US-09-264-737-1
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                                                                                                         APPLICANT: Feng, Paul C.C.
APPLICANT: Ruff, Thomas G.
TITLE OF INVENTION: Engineering Plant Resistance to Pyridines
TITLE OF INVENTION: Expression of Esterase Enzymes
FILE REFERENCE: 38-21(10551) RLE3 Pyridine Tolerance
CURRENT APPLICATION NUMBER: US/09/264,737A
CURRENT APPLICATION NUMBER: US/09/264,737A
CURRENT FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: 60/077,377
EARLIER FILING DATE: 1998-03-10
NUMBER OF SEQ ID NOS: 11
SOPTWARE: Patentin Ver. 2.0
LENGTH: 530
                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09264737A Patent No. 6107549
                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local Similarity
   Query Match
                                                       LENGTH: 539
TYPE: PRT
ORGANISM: Rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVPYIVGINKQEFGWLLPTMMGFPLSEGKLDQKTATSLLWKS-----YPIANI----PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AIPSIIGVNNHECGFLLP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KPPLGSLRFAPPQPAEPWSFVKNTTSYPPMCCQDPVVEQMTSDLFTNFTGKERLTLEF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLGSLRFTNPQPASPWDNLREATSYPNLCLQNS--EWLLLD------QHMLKVHYPK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WLLPLVLTSLASSATW--AGQPASPPVVDTAQGRVLGKYVSLEGLAFTQPVAVFLGVPFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TFARTGUPUGUDLSLWP--AYNLTEQYLQLDLWMSLGQRLKEPRVDFWTSTI 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QYRPSFSSDKFTKPKTVIGDHGDEIFSVFGFPLLKGD-----APEEEVSLSKTVMKFWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RHRPQCFED--TKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMKYWA
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ilarity 43.8%;
Conservative (
   33.6%;
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Pred. No. 7.4e-110;
3; Mismatches 191;
   Score 1034.5;
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Length 539;
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 DQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EATSYPNLCLQNSEWLLLDQHML------KVHYP-KFGVSEDCLYLNIYAPAHADTGSK 143
                                                                            LGORLKEPRVDFWT 546
                                                                                                                                      LKGDIVMFEGATEEEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMS
                                                                                                                                                                          LADLLFGVPSVNVARHHRDAGAPTYMYEYRYRPSFSSDMRPKTVIGDHGDEIFSVLGAPF
                                                                                                                                                                                                                                                                                                   GDPKENTAFLTTVIDGVLLPKAPAEIYEEKKYNMLPYMVGINQQEFGWIIPMQMLGYPLS
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                                               AAQKLKDKEVAFWT 521
                                                                                                                                                                                          LGDVFFVVÞALITARYHRDAGAÞVYFYEFRHRÞQCFEDTKÞAFVKADHADEVRFVFGGAF 472
                                                                                                                                                                                                                                      EGKLDQKTATELLWKS-----YPIVNVSKELTPVATEKYLGGTDDPVKKKDLFLDM
                                                                                                                                                                                                                                                                                                                                                                 SSL----FRKNTKSLAEKIAIEAGCKTTTSAVMVHCLROKTEEELMEVTLKMKFMALDLV
                                                                                                                                                                                                                                                                                                                                                                                                                               FLVAVNRWVQDNIANFGGDPGSVTIFGESAGGQSVSILLLSPLTKNLFHRAISESGVALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPVMVWIHGGGLMVGGASTYDGLALSAHENVVVVTIQYRLGIGGFGFNIDE-----L 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSAP-PVVDTVKGKVLGKFVSLEGFAQPVAVFLGVPFAKPPLGSLRFAPPQPAESWSHVK
                                                                                                                                                                                                                                                                    -----KEAPEILSGSNKSLALHLIQNILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDL
                                                                                                                                                                                                                                                                                                                                  -TKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPM------
                                                                                                             EGATEEEIKLSKMVMKYWANFARNGNPNGEGLPQWPAYDYKEGYLQIGATTQ
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'1; Mismatches 176;
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Sequence 26, Apprise No. 6001625
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GENERAL INFORMATION:
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTOREY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc
                                                                                                                                                                                                                                                                               STREET: 9669 /
                                                                                                                                                                                                                             COUNTRY: US
ZIP: 22031
                                                                                                                                                                                                                                                             STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application
                                                                                                                                                                                                                                                                                                    9669 A Main Street, P.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Broomfield, Clarence
                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08446100
                                                                                              US/08/446,100
                                                                                                                                                                                                                                                                                                                                                                              Mutagenesis
                                                                                                                                     Version
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Query Match

LENGTH: TYPE: a

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RESULT 14
US-08-446-100-28

Sequence 28, Application US/08446100
Patent No. 6001625
GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: human esterases US-08-446-100-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity Matches 200; Conserv
                           COUNTRY: US
ZIP: 22031
COMPUTER READABLE FORM:
                                                                      Automotion STREET: you CITY: Fairfax
                                                                                                                                       NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks
                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: YE ANTI-SENSE: YES FRAGMENT TYPE: NORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                 523 QYLQLDLNMSLGQRLKEPRVDFWTS 547
                                                                                                                                                                                                                                                                                                                                                                            412 GYLQIGANTQAAQKLKDKEVAFWTN 436
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                                                                                                               E: Hendricks and Assoc.
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                                                                                                                                                                 Lockridge, Oksana
VENTION: Site-Directed Mutagenesis
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                                                                                                                 Box 2509
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US-08-446-100-30
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Sequence 30, Application US/08446100
Patent No. 6001625
GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence
APPLICANT: Millard, Charles B
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INFORMATION FOR SEQ ID NO:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
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ANTI-SENSE: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: human esterase
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LENGTH: 454 amino acids
TYPE: amino acid
STRANDEDNESS: single
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NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: bro
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IFGFFTTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILS 244
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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Gaps

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120

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358

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; ORGANISM: human esterases US-08-446-100-30
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Best Local Similarity
Matches 200; Conserv
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INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: broo
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 425-4250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: YES
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
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STREET: 9669 A Main Street, P.O. Box 2509
CTTY: Fairfax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
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523 QYLQLDLNMSLGQRLKEPRVDFWTS 547
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                                          ELFSVFGAPFLK-----EGASEEEIRLSKMVMKFWANFARNGNPNGKGLPHWPEYNQKE
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nilarity 44.9%;
Conservative 64
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t; Pred. No. 9.5e-94;
64; Mismatches 150;
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Search completed: June 16, 2005, 20:46:37 Job time : 46 secs

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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                           score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                    2915
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2607.5
2606
2597.5
2598.5
2588.5
                                                                                                                                                                                                                                            Score
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100.0
100.0
94.7
94.2
84.7
84.6
84.4
84.4
79.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    June 16, 2005, 20:45:08 ; Search time 158 Seconds (without alignments)
1411.975 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
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3079
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12:
13:
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:/cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pep:*
:/cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*
:/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
:/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
:/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
:/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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:/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
:/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
:/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
:/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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:/cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
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:/cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
:/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
:/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
:/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
:/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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US-10-757-262-46

US-10-451-168-91

US-10-431-256-10

US-10-431-168-92

US-10-0494-749-2375

US-10-114-270-196
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US-10-381-898-2
US-10-104-047-2219
US-10-233-933A-2
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                                                                                                                                                                                                                                          Description
                                                    Sequence 2, Appli
Sequence 2, Appli
Sequence 46, Appli
Sequence 91, Appl
Sequence 10, Appl
Sequence 92, Appl
Sequence 2375, Ap
Sequence 196, App
                  Sequence
Sequence
                  2, Appli
2219, Ap
Appli
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US-10-028-07/2-542 US-10-140-808-542 US-10-121-049-542 US-10-123-904-542 US-10-175-746-542 US-10-176-921-542 US-10-176-921-542 US-10-176-921-542 US-10-176-921-542 US-10-137-865-542 US-10-137-865-542 US-10-137-865-542 US-10-140-474-542 US-10-140-474-542 US-10-142-431-542 US-10-143-114-542 US-10-136-130-230 US-10-230-138-210 US-10-230-138-210 US-10-230-338-210 US-10-142-419-542 US-10-230-338-210 US-10-142-419-542 US-10-230-338-210 US-10-142-419-542 US-10-230-338-210 US-10-142-419-542 US-10-218-631-210	-10-233-933A-4 -10-451-168-93 -0-152-98-68 -10-162-806-68 -10-267-756-5 -10-858-271-28 -10-377-072-4 -10-377-072-4 -10-377-072-4 -10-373-836-23 -09-833-245-10
Sequence 342, Appl Sequence 542, App Sequence 210, App Sequence 23, Appl Sequence 542, App Sequence 542, App Sequence 542, App Sequence 542, App Sequence 542, App Sequence 542, App Sequence 540, App Sequence 541, App Sequence 542, App Sequence 542, App Sequence 543, Appl Sequence 540, App Sequence 541, App Sequence 542, App Sequence 542, App Sequence 543, Appl Sequence 543, Appl	400000 0000000000000000000000000000000

## ALIGNMENTS

```
APPLICANT: CURTLE, ROTY A. J.

APPLICANT: CURTLE, ROTY A. J.

APPLICANT: Silos-Santiago, Inmaculada

TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE

TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF

FILE REFERENCE: 10448-122001

CURRENT APPLICATION NUMBER: US/10/023,515

CURRENT FILING DATE: 2001-12-18

PRIOR APPLICATION NUMBER: 60/256,369

PRIOR APPLICATION NUMBER: 60/279,508

PRIOR APPLICATION NUMBER: 60/279,508

PRIOR APPLICATION NUMBER: 60/279,508

PRIOR FILING DATE: 2000-12-18

PRIOR APPLICATION NUMBER: 60/279,508

PRIOR FILING DATE: 2000-103-28

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                         LENGTH: 581
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-515-2
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US-10-023-515-2
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Publication No. US20020182636A1
GENERAL INFORMATION:
                                                                                                                                                                                              Query Match 100.0%; 9
Best Local Similarity 100.0%; 1
Matches 581; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 2
61 NVFLGVPFAAPPLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLLDQHMLKVHYPK 120
                                                                                                                   1 MPQGLTSSASQWCFFLILQPLLGHRQWGKTGPSAEGPORNTRLGWIQGKQVTVLGSPVPV 60
                                                                                   MPQGLTSSASQWCFFLILQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPV
                                                                                                                                                                                              Score 3079; DB 13; Length 581; Pred. No. 1.1e-277; Mismatches 0; Indels 0;
                                                                                                                                                                                                 0;
                                                                                                                                                                                                    Gaps
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APPLICANT: CULLIA, ROTY A. J.

APPLICANT: S1108-Santiago, Inmaculada

TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE

TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF

FILE REFERENCE: 10448-122001

CURRENT APPLICATION NUMBER: US/10/674,636

CURRENT FILING DATE: 2003-09-29

PRIOR PILING DATE: 2001-12-18

PRIOR FILING DATE: 2001-12-18

PRIOR FILING DATE: 2001-12-18

PRIOR FILING DATE: 2001-12-18

PRIOR FILING DATE: 2001-12-18

PRIOR FILING DATE: 2001-12-18

PRIOR FILING DATE: 2001-12-18

PRIOR FILING DATE: 2001-12-18

PRIOR FILING DATE: 2001-12-18

PRIOR FILING DATE: 2001-12-18

PRIOR FILING DATE: 2001-12-18

PRIOR FILING DATE: 2001-12-18

PRIOR FILING DATE: 2001-12-18

PRIOR FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                     ; SEQ ID NO 2;
LENGTH: 581
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-674-636-2
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US-10-674-636-2
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Best Local Similarity
Matches 581; Conserv
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Publication No. US20040086922A1
GENERAL INFORMATION:
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                                                                                                                     100.0%; Score 3079; DB 15; ilarity 100.0%; Pred. No. 1.1e-277; Conservative 0; Mismatches 0;
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                                           RVDFWTSTIPLILSASDMLHSPLSSLTFLSLLQPFFFFFCAP
                                                       RVDFWTSTIPLILSASDMLHSPLSSLTFLSLLQPFFFFFCAP 581
                                                                                      <u>EGATÉEEKLLSRKYMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEP</u>
                                                                                                  EGATEEEKLLSRKMKYWATFARTGNPNGNDLSLWPAYNLTEQYLOLDLNWSLGQRLKEP
                                                                                                                                   PALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMF
                                                                                                                                                                                               APEILSGSNKSLALHLIQNILHIPPQYLHLVANBYFHDKHSLTEIRDSLLDLLGDVFFVV
                                                                                                                                                                                 APEILSGSNKSLALHLIQNILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVV
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                                                                                                                                                                                                                                 KPSKELLTLSQKTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPMKE
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Sequence 46, Application US/10757262
Publication No. US20040197825A1
GENERAL INFORMATION:
APPLICANT: Klaricheti, Venkateswarlu
APPLICANT: Klaricheti, Venkateswarlu
APPLICANT: Eliaso-Santiago, Inmaculada
APPLICANT: Eliaso-Santiago, Inmaculada
TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
TITLE OF INVENTION: 33751, 52872, 14053, 20739, 22444, 43239, 4473, 51164,
TITLE OF INVENTION: 33751, 52872, 14053, 20739, 22444, 43239, 44733, 51164,
TITLE OF INVENTION: 33751, 52872, 14053, 20739, 22544, 4327, 52908, 69112, 14990,
TITLE OF INVENTION: 32720, 4809, 14303, 12366, 21165, 30911, 41897, 1171LE OF INVENTION: 32720, 4809, 14303, 12616, 17827, 32620, 577, 619, 1423,
TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 88203, 33278 OR
TITLE OF INVENTION: 53053, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
TITLE OF INVENTION: 53053, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
TITLE OF INVENTION: 50053, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
TITLE OF INVENTION: 50053, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
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TITLE OF INVENTION: 50053, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
TITLE OF INVENTION: 50053, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
TITLE OF INVENTION: 50053, 9626, 13231, 32409, 84260, 2882, 8203, 32678

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Sequence 91, Application US/10451168
PUDDICATION NO. US20040091969A1
GENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM p.l.c.
APPLICANT: SMITHKLINE BEECHAM p.l.c.
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: NOVEL COMPOUNDS
FILLS REFERENCE: GP50039
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: FCT/US01/49232
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: 60/260,482
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US-10-451-168-91
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NUMBER OF SEQ ID NOS: 136
SOFTWARE: FastSEQ for Windows
SEQ ID NO 46
LENGTH: 581
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Best Local S
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ORGANISM: Homo
-10-757-262-46
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                                                                                                                                                                                                                                                                                                                                          RVDFWTSTIPLILSASDMLHSPLSSLTFLSLLQPFFFFCAP 581
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                                                                                                                                                                                                                                                                                                                                                                                      EGATEEEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEP
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Pred. No. 1.1e-277;
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RESULT 5 US-10-433-256-10

485

Sequence 10, Application US/10433256
publication No. US20040081980A1
GENERAL INFORMATION:
APPLICANT: SANJANWALA, Madhusudan M.; YAO, Monic
APPLICANT: AU-YOUNG, Janice K.; BAUGHN, Mariah
APPLICANT: ARVZU, Chandra S.; RING, Huijun Z.
APPLICANT: LEE, Ernestine A.; DING, Li

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; SEQ ID NO 91
; LENGTH: 575
; TYPE: PAT
; ORGANISM: HOMO 5
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Matches 553; Conserv
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SOFTWARE: FastSEQ for Windows
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OR APPLICATION NUMBER: 60/264,922
OR FILING DATE: 2001-01-30
OR FILING DATE: 2001-02-06
OR FILING DATE: 2001-02-06
OR APPLICATION NUMBER: 60/276,988
OR APPLICATION NUMBER: 60/281,535
OR APPLICATION NUMBER: 60/281,535
OR APPLICATION NUMBER: 60/289,622
OR FILING DATE: 2001-04-04
OR APPLICATION NUMBER: 60/289,622
OR FILING DATE: 2002-06-28
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                                                                                                                                                                LALHLIQNILHIPPQYLHLVANEYFHDKHSLTBIRDSLLDLLGDVFFVVPALITARYHRD
                                                                                                                                                                                                KTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPMKEAPEILSGSNKS
                                                                                                                                                                                                                                                                                                                 WDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPWAKGLF
                                                                                                                                                                                                                                                                                                                                                    IYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTT 191
                                                                                                                                                                                                                                                                                                    WDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLF
ILSASDMLHSPLSSLTFLSLLQPFFFFCAP
              | ILSASDMLHSPLSSLTFLSLLQPFFFFCAP
                                                 RKMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIPL
                                                               RKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIPL
                                                                                               AGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGD1
                                                                                                              AGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLS
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ilarity 97.0%;
Conservative
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Pred. No. 2.1e-262;
3; Mismatches 6;
 575
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TITLE OF INVESTIGN, CIAIG H.

TITLE OF INVESTIGN ENGREMENT SPECIAL PROBLEM STATEMENT OF STATEMENT APPLICATION NUMBER: US/10/433,256

CURRENT APPLICATION NUMBER: US/10/433,256

CURRENT FILING DATE: 2003-05-30

PRIOR APPLICATION NUMBER: PCT/US01/47429

PRIOR FILING DATE: 2001-12-04

PRIOR APPLICATION NUMBER: US 60/254,308

PRIOR APPLICATION NUMBER: US 60/256,189

PRIOR FILING DATE: 2000-12-15

PRIOR FILING DATE: 2000-12-15

PRIOR PRILING DATE: 2000-12-13

PRIOR PRILING DATE: 2000-12-13

PRIOR APPLICATION NUMBER: US 60/262,706

PRIOR FILING DATE: 2000-10-19

PRIOR APPLICATION NUMBER: US 60/262,706

PRIOR APPLICATION NUMBER: US 60/262,706

PRIOR APPLICATION NUMBER: US 60/266,020

PRIOR FILING DATE: 2001-01-19

PRIOR PRILING DATE: 2001-02-02

NUMBER OF SEQ ID NOS: 26

SOPTWARE: PERL PROGram

LENGTH: 642
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; OTHER INFORMATION: Incyte ID No: 6538080CD1
US-10-433-256-10
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Matches 548; Conserva
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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                                            DISIMPAYNITEQYIQIDINMSIGQRIKEPRVDFWTSTIPLIISASDMIHSPISSITEIS
                                                                                                                                     TKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEBEKLLSRKWMKYWATFARTGNPNGN
                       DLFLWPAYNLTEQYLQLDLNMSLGQRLKEPRVEFWTSTIPLILSASDMLHSPLSSLTFLS
                                                                                                           TKPAFVKADHADEVRFVFGGAFLKGDÍVMFEGATBEEKLLSRKVMKYWATFARTGNENGN
                                                                                                                                                                                               VANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYBFRHRÞQCFED
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YUE, Henry; TRIBOULEY, Catherine M.
LU, Dyung Aina M.; LAL, Preeti G.
WARREN, Bridget A.; YANG, Junming
CHAWLA, Narinder K.; NGUYEN, Danniel B.
GANDHI, Ameena R.; LU, Yan
ISON, Craig H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.2%;
ilarity 99.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2900; DB 15;
Pred. No. 6.3e-261;
2; Mismatches 1;
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PRIOR FILING DATE: 2001-03-19
PRIOR FILING DATE: 2001-04-04
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/289,622
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FastSEQ for Windows Version (SEQ ID NO)
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-451-168-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/US01/49232
PRIOR FILING DATE: 2000-12-17
PRIOR PILING DATE: 2000-12-17
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR APPLICATION NUMBER: 60/260,482
PRIOR APPLICATION NUMBER: 60/260,482
PRIOR PILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR APPLICATION NUMBER: 60/264,797
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR APPLICATION NUMBER: 60/266,797
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US-10-451-168-92
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Publication No. US20040091969A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NOVEL COMPOUNDS FILE REFERENCE: GP50039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SMITHKLINE BEECHAM CORPORATION APPLICANT: SMITHKLINE BEECHAM p.l.c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                 246
                                                                                                                                                                                                                                     186
                                                                                                                                                                                                                                                   192 WDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPWAKGLF 251
                                                                                                                                                                                                                                                                                                                                     132 IYAPAHADTGSKLFVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTT 191
                                                                                                                                                                                                                                                                                                                                                                                                                  99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 WAIWVLAAP-----TKGPSAEGPORNTRLGWIOGKQVTVLGSPVPVNVFLGVPFAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                72 PLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHNLKVHYPKFGVSEDCLYLN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 WCEFLILOPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVVPLGVPFAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             499;
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KSLAL-----HLIQNILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALI
                                                                          KTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPMKE--APEILSGSN
                                                                                                                                HKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQ 305
                                                                                                                                                               HKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSBALLRCLRTKPSKELLTLSQ 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 84.7%;
Similarity 91.4%;
                                            KTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPMVRILAVHTATPSN
                                                                                                                                                                                                                       WDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLF
                                                                                                                                                                                                                                                                                                             IYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTT
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APPLICANT: SEKI, NACHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: NAGHIKA, KENJI
APPLICANT: NAGHIKA, KENJI
APPLICANT: NAGHIKA, KENJI
APPLICANT: NASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
FILE REFERENCE: 08435/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: DP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATENTIAN SECTION NUMBER: 1380
SOFTWARE: PATENTIAN SECTION NOS: 3375
LENGTH: 525
LENGTH: 525
TYPE: PRT
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10-094-749-2375
                                                                                                                                                                                                                                                                              B4.6%;
Local Similarity 90.9%;
les 501; Conservarion
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                       211
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OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
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                                                                                                                                                             REATSYPNICLQNSEWLLLDQHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVWF 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTSUKA, KAORU
NAGAI, KEIICHI
IRIE, RYOTARO
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WVQXWIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIFYLEAHD
                                                                                 PGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALS
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                                                                                                                                   REATSYPHICLONSEWLLLDQHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVWF
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                                                           PGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALS
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YAMAMOTO, JUN-ICHI
ISONO, YUUKO
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                                                                                                                                                                                                                                                                                      Score 2606; DB 15;
Pred. No. 1.2e-233;
0; Mismatches 0;
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             APPLICANT: Padigaru, Muralidhara
APPLICANT: Shimkete, Richard A.
APPLICANT: Shimkete, Richard A.
APPLICANT: Gangolli, Esha A.
APPLICANT: Taupier Jr., Raymond J.
APPLICANT: Casman, Stacie J.
APPLICANT: Liete, Mario W.
APPLICANT: Liete, Mario W.
APPLICANT: Liete, Mario W.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Stone, David J.
APPLICANT: Stone, David J.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Rothenberg, Mark E.
TITLE OF INVENTION: NO. US20040030110Alel Proteins and Nuc
FILE REFERENCE: 21402-322C
CURRENT APPLICATION NUMBER: 60/281,086
PRIOR APPLICATION NUMBER: 60/281,086
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR FILLING DATE: 2001-04-03
PRIOR FILLING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR APPLICATION NUMBER: 60/281,863
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US-10-114-270-196
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Kekuda, Ramesh
Miller, Charles E.
Malyankar, Uriel M.
Spytek, Kimberly A.
                                                                                                                                                                                                                                                                                                                                                                                                       Pena, Carol E.A.
Smithson, Glennda
Burgese, Catherine E.
Gerlach, Valerie
Padigaru, Muralidhara
Shimkete, Richard A.
Gangolli, Esha A.
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Liu, Ziaohong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vernet, Corine
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D. US20040030110A1
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PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/282,020
PRIOR PRIOR APPLICATION NUMBER: 60/282,930
PRIOR PRIING DATE: 2001-04-10
PRIOR PRIING DATE: 2001-04-10
PRIOR PILING DATE: 2001-04-10
PRIOR PILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/283,512
PRIOR PILING DATE: 2001-04-12
PRIOR PRIING DATE: 2001-04-13
PRIOR PRIING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-13
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PRIOR PIL
                                            Sequence 2, Application US/10381898
Publication No. US20040086887A1
GENERAL INFORMATION:
APPLICANT: AZIMZAI, Yalda; BAUGHN, Mariah R.;
APPLICANT: BOROWSKY, Mark L.; DING, Li;
APPLICANT: DUGGAN, Brendan; ELLIOTT, Vicki S.;
APPLICANT: GANDHI, Ameena R.; GRIFFIN, Jennifer;
APPLICANT: HAPALIA, April J.A.; ISON, Craig H.;
APPLICANT: KHAN, Farrah A.; LAL, Preeti G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331 DLLSQKAFKAIPSIIGVNNHECGFLLPMKE--APEILSGSNKSLAL-----HLIQNILHI
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Similarity 94.3%;
97; Conservative
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Pred. No. 8.8e
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.8e-233;
es 17; Indels
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APPLICANT: ARVIZU, Chandra S.; POLICKY, Jennifer L.;
APPLICANT: SANJANWALA, Madhusudan M.;
APPLICANT: TANG, Y. Tom, TRIBOULEY, Catherine M.;
APPLICANT: CHAWLA, Narinder K.; WALSH, Roderick T.;
APPLICANT: WARREN, Bridget; XU, Yuming;
APPLICANT: WARREN, Bridget; XU, Yuming;
APPLICANT: WARREN, Unming; YAO, Monique; YUE, Henry
TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
FILE REFERENCE: PI-0233 USN
CURRENT APPLICATION NUMBER: US/10/381,898
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: PCT/US01/30662
PRIOR APPLICATION NUMBER: US 60/236,947
PRIOR APPLICATION NUMBER: US 60/236,947
PRIOR APPLICATION NUMBER: US 60/236,947
PRIOR APPLICATION NUMBER: US 60/238,864
PRIOR APPLICATION NUMBER: US 60/242,323
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 60/247,581
PRIOR APPLICATION NUMBER: US 60/247,581
PRIOR APPLICATION NUMBER: US 60/247,581
PRIOR APPLICATION NUMBER: US 60/249,519
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PRIOR APPLICATION NUMBER: US 60/249,519
PRIOR APPLICATION NUMBER: US 60/252,834
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: US 60/252,834
PRIOR FILING DATE: 2000-11-30
NUMBER: US 60/252,834
PRIOR APPLICATION NUMBER: US 60/252,834
PRIOR APPLICATION NUMBER: US 60/252,834
PRIOR APPLICATION NUMBER: US 60/250,567
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PERL PROGram
PRIOR APPLICATION NUMBER: US 60/250,567
PRIOR APPLICATION NUMBER: US 60/250,567
PRIOR APPLICATION NUMBER: US 60/250,567
PRIOR APPLICATION NUMBER: US 60/250,567
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; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7473645CD1
US-10-381-898-2
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TKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKVMKYWATFARTGNPNGN
                                                                                             VANEYFHDKHSLÍTBÍRDSLLDLLGDVFFVVÞALÍTARYHRDAGAÞVYFYBFRHRÞQCFED
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Similarity 94.4%;
                                                                                                                             VANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEFRHRBQCFED
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Pred. No. 6.6e.
1; Mismatches
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Query Match Best Local S Matches

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RESULT 9 US-10-381-898-2

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US-10-104-047-2219
; Sequence 2219, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20030236392A1e1 full ler
FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT APPLICATION NUMBER: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE: 2002-03-25
; PRIOR FILING DATE: 2002-03-25
                                                                                                                                      RESULT 11
US-10-233-933A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2219
                                                                               Sequence 2, Application US/10233933A Publication No. US20040214171A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
APPLICANT: Yamashita, Tetsuro
APPLICANT: Miyazaki, Masao
TITLE OP INVENTION: CAT KIDNEY DISEASE MARKER
FILE REFERENCE: SHIG FP02US006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 469
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Pred. No. 1.5e-219;
2; Mismatches 0;
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              APPLICANT: YAMASHITA, Tetsuro
APPLICANT: Miyazaki, Masao
TITLE OF INVENTION: CAT KIDNEY DISEASE MARKER
FILE REFERENCE: SHIG FP02US006
CURRENT APPLICATION NUMBER: US/10/233,933A
CURRENT FILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: JP2002-057908
PRIOR APPLICATION NUMBER: JP2002-057908
IPRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 4
LENGTH: 542
TYPE: PRT
ROANISM: Felis Catus
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      US-10-233-933A-4
                                                                                                                                                                                                                                                                                                Sequence 4, Application US/10233933A Publication No. US20040214171A1 GENERAL INFORMATION:
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Best Local
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PRIOR APPLICATION NUMBER: JP2002-057908
PRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Felis
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EGVPLWPAYTQSEQYLKLDLSVSVGQKLKEQEVEFWMNTI 540
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PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR APPLICATION NUMBER: 60/289,622
PRIOR APPLICATION NUMBER: 60/289,622
PRIOR FILING DATE: 2002-06-28
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US-10-451-168-93
                                                                                                                                                                                                           FILE REFERENCE: GP50039

CURRENT APPLICATION NUMBER: US/10/451,168

CURRENT FILING DATE: 2003-11-12

PRIOR APPLICATION NUMBER: PCT/US01/49232

PRIOR FILING DATE: 2000-12-17

PRIOR APPLICATION NUMBER: 60/256,710

PRIOR FILING DATE: 2000-12-19

PRIOR APPLICATION NUMBER: 60/257,048

PRIOR APPLICATION NUMBER: 60/257,048

PRIOR APPLICATION NUMBER: 60/250,482

PRIOR APPLICATION NUMBER: 60/260,482

PRIOR APPLICATION NUMBER: 60/260,482

PRIOR APPLICATION NUMBER: 60/260,482

PRIOR FILING DATE: 2001-01-09
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Publication No. US20040091969A1
GENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM P.1.C.
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: NOVEL COMPOUNDS
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ID NOS: 110
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; ORGANISM: Homo sapie
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: X
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: X
US-09-925-298-689
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; TYPE: PRT
; ORGANISM: Homo s
US-10-451-168-93
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LENGTH: 549
                                                                     Matches
                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Publication No. US20
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 689,
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA103
CURRENT APPLICATION NUMBER: US/09/925,298
CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 93
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                                                                                  Local
16 GQDSASPIRTTHTGQVLGSLVHVKGANAGVQTFLGIPFAKPPLGPLRFAPPEPPESWSGV
                 l Similarity
248; Conserv
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o. US20020039764A1
                                                                  Conservative
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                                                                                                                                                                                         Xaa equals
                                                                             39.9%; Score 1230; DB 9; 46.7%; Pred. No. 2.6e-105;
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                                                                Mismatches
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GENERAL INFORMATION:

APPLICANT: ROSEN et al.

FITLE OF INVENTION: Nucleic Acids, Proteins and Ani
FILE REFERENCE: PA103PLC1

CURRENT APPLICATION NUMBER: US/10/102,806

CURRENT FILING DATE: 2002-03-22

FRIOR APPLICATION NUMBER: 09/925,298

PRIOR APPLICATION NUMBER: PCT/US00/05881

PRIOR APPLICATION NUMBER: PCT/US00/05881

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR APPLICATION NUMBER: 60/124,270
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US-10-102-806-689
US-10-102-806-689, Application US/10102806
Sequence 689, Application US/10102806
Dublication US/20030054421A1
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SOFTWARE: PatentIn Ver. 2.
SEQ ID NO 689
LENGTH: 549
                                                                                                                   Matches
                                                                                                                                                     Query Match
                                                                                                                                                                                                TYPE: PRITTYPE: PRITTYPE: ORGANISM: Homo sapiens
PRATTYRE:
NAME/KEY: SITE
LOCATION: (1)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (7)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                     Local Similarity
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                                                                          GPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAPPLGSLRFTNPQPASPWDNL
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REATSYPHICLON----SEWLLLDQHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EFOHOPSWLKNIRPPHMKADHGDELPFVF-RSFFGGNYIKF---TEEEEQLSRKMMKYWA
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                                      GQDSASPIRTTHTGQVLGSLVHVKGANAGVQTFLGIPFAKPPLGPLRFAPPEPPESWSGV
                                                                                                                   Conservative
                                                                                                                 39.9%; Score 1230; DB 14;
46.7%; Pred. No. 2.6e-105;
vative 91; Mismatches 168;
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LEAHDYEKSEDL--QVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGA 323
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                                                                 EFOHOPSWLKNIRPPHMKADHGDELPFVF-RSFFGGNYIKF---TEEEEQLSRKMMKYWA
                                                                                 EFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKWMKYWA 499
                                                                                                                             LLMLPPTFGDLLREEYIGUNGDPQTLQAQFQEMMADSMFVIPALQVAHF-QCSRAPVYFY
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Matches 581
            14-JAN-2004; 2004WO-US000750.
                                                           WO2004065576-A2
                                                                                                       urological disorder; uropathic; cytostatic; benign prostatic hyperplasia; human.
                                                                                                                                            Human urological disorder
                                                                                                                                                                                                                   ADQ89094 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                related disorders. A claimed method of treating or preventing a disorder (especially a pain-related disorder) characterised by aberrant activity of a 53010-expressing cell involves administering a compound that modulates 53010 activity or expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes the use of polypeptides related to CC urological disorders for identifying a compound capable of treating a CC urological disorder, identifying a subject having a urological disorder, contracting a subject having a urological disorder. Also described: (1) a method for identifying a compound capable of treating a urological CC disorder; (2) a method for identifying a subject having a urological CC disorder; and (3) a method for treating a subject having a urological CC disorder. The compound has uropathic and cytostatic activities. The CC compound capable of treating a urological disorder in the compound capable of treating a urological disorder. Disorders include urinary incontinence and benign prostatic CC thyong a urological disorder, or treating a subject having a urological conformation. The present sequence represents a human urological disorder crelated protein, which is used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Simi
Matches 581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-TAN-2003;
04-FEB-2003;
27-MAR-2003;
08-MAY-2003;
19-MAY-2003;
16-JUN-2003;
16-JUL-2003;
30-JUL-2003;
26-SEP-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of polypeptides related to urological disorders, e.g. 44390, 5. 211 or for identifying a compound capable of treating a urological disorder or identifying and treating a subject having a urological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
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DB; ADQ89093.
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APEILSGSNKSLALHLIQNILHIPPQYLHLVANEYFHDKHSLTBIRDSLLDLLGDVFFVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                 KPSKELLTLSQKTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPMKE
                                                                                                                                 LILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRT
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                                               KPSKELLTLSQKTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPMKE
                                                                                                               LILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRT
                                                                                                                                                                           YRLGIFGFFTTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSS
                                                                                                                                                                                                 YRLGIFGFFTTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSS
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2003US-0447783P.

2003US-0457901P.

2003US-0468775P.

2003US-0471614P.

2003US-0471614P.

2003US-0478742P.

2003US-0488529P.

2003US-049154P.

2003US-0499594P.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-DEC-2000;
09-JAN-2001;
30-JAN-2001;
                                                                                                                                                                                                                                    Agarwal P,
Martensen
              Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder
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08-MAY-2001;
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19-MAR-2001;
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GLAXO GROUP
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; 2000US-0256048P.
; 2001US-026048P.
; 2001US-0264922P.
; 2001US-026492P.
; 2001US-0276988P.
; 2001US-0276988P.
; 2001US-0281535P.
; 2001US-0289622P.
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CC cardiant, antiulcer, virucide, antithyroid, cerebroprotective, anorectic, and metabolic. Polypeptides and polynucleotides of the invention are CC useful in the treatment, or as a vaccine in the prevention of, cancer, CC wound healing disorders, infection, atherosclerosis, Parkinson's disease CC and Alzheimer's disease, autoimmune disorder, haematopoletic disorder, inflammation, neoplastic diseases, nervous system related disorders and CC cardiovascular disorders, pancreatitis, respiratory disorder, CC disordership, systemic autoimmune disease, hyper-immunity, CC developmental abnormality, gastrointestinal ulceration, neuropathy, CC disorders e.g. hypothyroidism, brain damages, colitis, cone photo-
CC transduction deficiency, neurological diseases, sperm dysfunction, thyroid culation disorders, diseases in the spinal cord, thyroid gland, heart, crachea, thymus, lymph node and muscular system, obesity, anorexia, CC growth abnormalities, and alleviation of precocious puberty. The CC sequences given in records ABP60965-ABP61019 represent novel human CC proteins of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated polypeptide with signal sequences which allow it to be secreted extracellularly or membrane associated. The activity of polypeptides of the invention may be described as, cytostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic, neuroprotective, immunosuppressive, haemostatic, antiniflammatory, neuroprotective, immunosuppressive, haemostatic, antiniflammatory,
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Matches 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy.
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24-JAN-2002; 2002US-0350435P.
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Yoshikawa
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Isono Y,
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Otsuka M, Nagahari K, Masuho Y;
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Query Match Best Local Similarity

67.3%; 100.0%;

Score 391; Pred. No.

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Sequence

642 AA;

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                    The invention relates to novel diagnostic and therapeutic polynucleotides celected from one of the 2722 sequences defined in the specification. A CC polynucleotide of the invention may have a use in gene therapy. The human CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be CC with human molecules, e.g. cell proliferative disorders associated autoimmune/inflammatory disorder, developmental disorders, or CC disorder, neurological disorders, gastrointestinal disorders, or CC disorder, neurological disorders, gastrointestinal disorders, or CC disorder, neurological disorders, pastrointestinal disorders, or CC molecules may also be used in genetic mapping, in identifying individuals CC from minute biological samples, in detecting single nucleotide CC gene therapy. The present sequence represents a dithp protein of the CC invention. Note: The sequence data for this patent is not represented in CC the printed specification, but was obtained in electronic format directly XX
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Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietze,
Patury S, Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schmidt JP,
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anticonvulsant; nootropic; enzyme; DME-10.
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Best Local S
Matches 481
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21-DEC-2000;
19-JAN-2001;
02-FEB-2001;
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Lee EA, Ding L, Ha
Lal PG, Warren BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and its nucleotide. DME is useful for diagnosing, treating or prevent disorders associated with aberrant expression of DME, where the disorder selected from autoimmune/inflammatory disorder such as acquired immunodeficiency syndrome (AIDS), asthma, atherosclerosis, psoriasis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human drug metabolizing polypeptide, useful in diagnosis, prevention or treatment of autoimmune/inflammatory, cell proliferative, neurological, developmental, endocrine, metabolic and gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 65; Page 155-156; 169pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-519668/55.
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                                                                                                                                                                                                                                                                 REATSYPULCLQUSEWILLLDQHMLKVHYPKFGVSEDCLYLUIYAPAHADTGSKLPVLVWF 150
                                                                                                                                                                                                                                                                                                                                                                                      GPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAPPLGSLRFTNPQPASPWDNL
                                      WVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIFYLEAHD
                                                                                                                                                                                                                                                                                                                                                  GPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAPPLGSLRFTNPQPASPWDNL
                                                                                                                                                        PGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALS
                                                                                                                                                                                                                                   REATSYPHICLONSEWILLIDOHMIKVHYPKFGVSEDCLYLNIYAPAHADTGSKIPVLVWF
                                                                                                                    PGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALS
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2000US-0257713P.
2001US-0262706P.
2001US-0266020P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to an isolated human drug metabolising enzyme (DME) ME is useful for diagnosing, treating or preventing
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a AJA, Tang YT, Yue H,
g J, Walia NK, Nguyen D
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Tribouley
DB, Gandhi
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RESULT 7
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W antiinflammatory; cardiant; antiulcer; virucide; antithyroid;
W cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;
W wound healing disorders; atherosclerosis; Parkinson's disease;
Alzheimer's disease; autoimmune disorder; haematopoietic disorder;
W inflammation; neoplastic disease; nervous system disorder;
W cardiovascular disorders; pancreatitis; respiratory disorder;
W hyperproliferation; systemic autoimmune disease; hyper-immunity;
W haematological disease; metabolic disease; permit systemic autoimmune disease; hyper-immunity;
W haematological disease; metabolic disease; sperm dysfunction;
W thyroid disorder; hypothyroidism; brain damage; colitis;
W thyroid disorder; hypothyroidism; brain damage; colitis;
W angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart;
W traches; thymus; lymph node; muscular system; obesity; anorexia;
W growth abnormality; precocious puberty.
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20-DEC-2000; 2000US-0257048P.
09-JAN-2001; 2001US-0264922P.
30-JAN-2001; 2001US-0264922P.
06-FEB-2001; 2001US-026492P.
19-MAR-2001; 2001US-026898P.
04-APR-2001; 2001US-0289522P.
WPI; 2002-508784/54.
N-PSDB; ABQ86171.
                                                                                                       Agarwal P,
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                                                                           SK,
                                                                      Cogswell JP, Kabnick
Smith RF, Strum JC,
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                                                                      ΧΈς,
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CC cardiant, antiulcer, virucide, haemostatic, antiparkinsonian, nootropic, cardiant, antiulcer, virucide, antithyroid, cerebroprotective, anorectic, cc cardiant, antiulcer, virucide, antithyroid, cerebroprotective, anorectic, cc diseful in the treatment, or as a vaccine in the prevention are cc wound healing disorders, infection, atherosclerosis, Parkinson's disease cand Alzheimer's disease, autoimmune disorder, haematopoietic disorders and cc ardiovascular disorders, nervous system related disorders and cc diviperproliferation, systemic autoimmune disease, hyper-immunity, cc developmental abnormality, gastrointestinal ulceration, thyroid cardiovascular diseases, merabolic diseases, byter remunity, con ephoto-cc disorders e.g. hypothyroidism, brain damages, colitis, cone photo-cc disorders e.g. hypothyroidism, brain damages, colitis, cone photo-cc dransduction deficiency, neurological diseases, stroke, anglogenesis, cc trachea, thymus, lymph node and muscular system, obseity, anorexia, cc growth abnormalities, and alleviation of precocious puberty. The sequences given in records ABP60965-ABP61019 represent novel human cc proteins of the invention
The invention relates to an isolated polypeptide with signal sequences which allow it to be secreted extracellularly or membrane associated. The activity of polypeptides of the invention may be described as, cytostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropicytostatic, antiparkinsonian, nootropicytostatic, vulnerary, antiparkinsonian, nootropicytostatic, vulnerary, antiparkinsonian, nootropicytostatic, vulnerary, antiparkinsonian, nootropicytostatic, vulnerary, antiparkinsonian, nootropicytostatic, antiparkinsonian, nootropicytostatic, vulnerary, antiparkinsonian, nootropicytostatic, antiparkinsonian, nootropicytostatic, antiparkinsonian, nootropicytostatic, antiparkinsonian, nootropicytostatic, antiparkinsonian, nootropicytostatic, antiparkinsonian, nootropicytostatic, antiparkinsonian, nootropicytostatic, antiparkinsonian, nootropicytostatic, antiparkinsonian, nootropicytostatic, no otropicytostatic,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1(a); Page 315; 335pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorder
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Query Match
Best Local Similarity
Matches 340; Conserv Sequence 356 AA; 58.5%; Score 340; 100.0%; Pred. No. B 5; Length 356;

Conservative

Ś В δ 밁 Ş 밁 S 밁 Ś 밁 S 317 482 197 422 137 362 302 242 77 17 VDFWTSTIPLILSASDMLHSPLSSLTFLSLLQPFFFFFCAP 581 GATEEEKLLSRKMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPR 541 VDFWTSTIPLILSASDMLHSPLSSLTPLSLLQPFFFFCAP 356 GATEEEKLLSRKYWKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNWSLGQRLKEPR ALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFE PEILSGSNKSLALHLIQNILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVP PEILSGSNKSLALHLIQNILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVP PŚKELLTLŚĆKTKŚFTRVVDGAFFPNEPLDLLSĆKAFKAIPSIIGVNNHECGFLLPMKEA PSKELLTLSQKTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPMKEA 361 ILSPMAKGLFHKAIMESGVAIIFYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRTK ILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRTK 301 0, red. No. 0; Mismatches 0; Indels 0 Gaps 256 481 196 421 136 76

ADB64065 standard;

protein;

469

B

04-DEC-2003 (first entry)

Human protein encoded by clone BRAWH20021910.

RESULT 8
ADB64065
ID ADB6
XX
AC ADB6
XZ
DT 04-D
XX
DE Huma
XX
KW Huma Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction-related prot protein;

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The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel comprehences. Also claimed is a polypeptide encoded by the polynucleotide or its partial peptide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide competitive of the polynucleotide by contacting the polypeptide or peptide competitive with the antibody of the encoded protein, and observing the binding compressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesising the polynucleotide or as a probe competitive and an antisense polynucleotide. The oligonucleotide genes may be included in them, for developing a diagnostic marker or competitive for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell conscription-related proteins, disease-related proteins and genes are conding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours, The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence presented is a protein of the invention. Note: Some of the sequence data for this patent is not represented in the printed consciplination, but is based on sequence information supplied by the consideration of fice.
                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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25-JAN-2002; 2002US-00350978.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page; 222pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as targets of gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-450961/43
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Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAR-2002; 2002EP-00007401
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                                                                                                                                                                                                                                                                                113 MLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVMFPGGAFKTGSASIFDGSALAAYE
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                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Hio Y, Otsuka K, Nagai K, Irie R,
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                   Score 329; DB 7;
Pred. No. 8.5e-313;
0; Mismatches 1;
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mantiinflammatory; cardiant; antiilcer; virucide; antithyroid;

mattiinflammatory; cardiant; antiilcer; virucide; antithyroid;

mattiinflammatory; cardiant; antiilcer; virucide; antithyroid;

mattiinflammatory; cardiant; antivilcer; virucide; antithyroid;

mattiinflammatory; cardiant; anterosclerosis; Parkinson's disease;

mound healing disorders; atherosclerosis; Parkinson's disease;

mound healing disorders; atherosclerosis; Parkinson's disease;

matting disorder; atherosclerosis; Parkinson's disease;

matting disorder; pancreatitis; respiratory disorder;

matting disorders; pancreatitis; respiratory disorder;

matting disorders; pancreatitis; respiratory disorder;

matting disorders; pancreatitis; respiratory disorder;

matting disorders; pancreatitis; respiratory disorder;

matting disorder; systemic aucoimmune disease; hyper-immunity;

matting disorder; systemic aucoimmune disease; sperm dysfunction;

thyroid disorder; hypothyroidism; brain damage; colitis;

matting disorder; hypothyroidism; brain damage; colitis;

matting disorder; hypothyroidism; brain damage; colitis;

matting disorder; hypothyroidism; brain damage; colitis;

matting disorder; hypothyroidism; brain damage; colitis;

matting disorder; hypothyroidism; brain damage; colitis;

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matting disorder; disorder; hypothyroidism; brain damage; colitis;

matting disorder; hypothyroidism; brain disorder; hypothyroidism; bra
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09-JAN-2001;
30-JAN-2001;
06-FEB-2001;
19-MAR-2001;
04-APR-2001;
08-MAY-2001;
                                                                        Agarwal P,
Martensen S
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   WPI; 2002-508784/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-DEC-2000;
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                                                                                                                                                                                  SMITHKLINE BEECHAM
SMITHKLINE BEECHAM
GLAXO GROUP LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGORLKEPRV 430
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                                                                                                                                                                                                                                                                                                                              ; 2001US-0264922P.
; 2001US-0266797P.
; 2001US-0276988P.
; 2001US-0281535P.
; 2001US-0289622P.
                                                                                                          Birkeland
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2001US-0260482P
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                                                                           Cogswell JP, Kabnick
Smith RF, Strum JC,
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disorder

WO200281498-A2

sapiens.

hypertension; congenital heart defect; aortic stenosis; valve diseau atrial septal defect; atrioventricular canal defect; ductus arterio; pulmonary stenosis; subaortic stenosis; ventricular septal defect; tuberous sclerosis; scleroderma; atherosclerosis; infectious diseasu; obesity; anorexia; neurodegenerative disorder; Alzheimer's diseasu; parkkinson's diseasu; immune disorder; haemachilia.

lve disease; us arteriosus; defect; VSD;

disease;

haemophilia; hypercoagulation; Crohn's

cancer.

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RESULT 10
ABU54639
ID ABU544
XX
AC ABU54-
XC
DT 03-JU
XX
DE Human
XX
KW Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC The invention relates to an isolated polypeptide with signal sequences charlow it to be secreted extracellularly or membrane associated. The cytostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic, consupportective, immunosuppressive, haemostatic, antiinflammatory, condition may be described as, conceptor cardiant, antiulcer, vinucide, antithyroid, cerebroprotective, anorectic, cand metabolic. Polypeptides and polynucleotides of the invention are communicated, antithyroid, cerebroprotective, anorectic, cand metabolic. Polypeptides and polynucleotides of the invention are communicated as a vaccine in the prevention of, cancer, condition and the invention are a vaccine in the prevention of, cancer, condition and labelmer's disease, autoimmune disorder, haematopoletic disorder, and Alzheimer's disease, autoimmune disorder, haematopoletic disorder, cardiovascular disorders, pancreatitis, respiratory disorders and hyperproliferation, systemic autoimmune disease, hyper-immunity, confidency developmental abnormality, gastrointestinal ulceration, neuropathy, confidency neurological diseases, sperm dysfunction, thyroid disorders e.g. hypothyroidism, brain damages, colitis, cone photoculation deficiency, diseases in the spinal cord, thyroid gland, heart, convilation deficiency, and alleviation of precocious puberty. The covalences given in records ABB60965-ABB61019 represent novel human convention of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 328
                               Human NOVX polypeptide #98
Human; NOVX; metabolic disorder;
                                                                             03-JUN-2003
                                                                                                                  ABU54639;
                                                                                                                                                  ABU54639 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder
                                                                                                                                                                                                                                                325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1(a); Page 313-314; 335pp; English.
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                                                                                                                                                                                                                                           DLLSOKAFKAIPSIIGVNNHECGFLLPM
                                                                                                                                                                                                                                                                  DLLSQKAFKAIPSIIGVNNHECGFLLPM 358
                                                                                                                                                                                                                                                                                                            YEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEPL
                                                                                                                                                                                                                                                                                                                                     YEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEPL
                                                                                                                                                                                                                                                                                                                                                                                     WVQXNIEFFGGDÞSSVTIFGESÁGAÍSVSSLÍLSÞMAKGLFHKAIMESGVAÍÍÞÝLEÁHD
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                                                                       (first entry)
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                                                                                                                                                  protein;
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; Pred. No. 9.
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                                                                                                                                                                                                                                           352
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9.9e-312;
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Indels

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cardiomyopathy; diabetes;

Claim 1; Page 303; 666pp; English

New isolated NOVX polypeptide useful for treating atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorex neurodegenerative disorders, Alzheimer's disease and cancer.

324

Padigaru M, Sh Anderson DW, L Macdougall JR, Ellerman K;

2003-046858/04. DB; ABX72267.

Gorman, Patturajan M,

Gerlach

χ., Υ.

BD;

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19-UIV-2001

12-SEP-2001

25-SEP-2001

25-SEP-2001

27-SEP-2001

17-OCT-2001

14-NOV-2001

14-NOV-2001

14-NOV-2001

14-NOV-2001

21-NOV-2001

21-NOV-2001
                                                                                                                                                                                                                                                                                                                                                  10-ARR-2001;
12-APR-2001;
13-APR-2001;
17-APR-2001;
19-APR-2001;
20-APR-2001;
20-APR-2001;
23-APR-2001;
23-APR-2001;
24-APR-2001;
24-APR-2001;
25-APR-2001;
27-APR-2001;
29-MAY-2001;
19-UN-2001;
19-UN-2001;
                                                                                                                                                                 Guo
                                                                                                                                                                                    (CURA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-APR-2001; 2001US-0282020P
10-APR-2001; 2001US-0282930P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-APR-2002;
                                                                                            Kekuda R, Miller CE, Malyankar Un, Techm, Zerhusen Du, Jan M, Liu X, Gusev VY, Li L, Vernet CAM, Zerhusen Du, Jan M, Liu X, Gusev VY, Li L, Vernet CAM, Zerhusen G, Burgess CE, Gerlac L, Shenoy SG, Pena CEA, Smithson G, Burgess CE, Gerlac L, Shimkets RA, Gangolli EA, Taupier RJ, Casman SJ, M, Shimkets RA, Gangolli EA, Taupier RJ, Casman SJ, N DW. Leite MW, Rastelli L, Edinger SR, Stone DJ;
                                                                                                                                                                                   CURAGEN CORP.
                                                                                                                                                                                                    2001US-0324802P

2001US-0325684P

2001US-0330143P

2001US-0332131P

2001US-0332740P

2001US-0332779P

2001US-0332115P

2001US-0332115P

2001US-03457621P

2002US-03457631P

2002US-03457631P

2002US-03457631P

2002US-03457631P
                                                                                                                                                                                                                                                                                                                  2001US-0282934P.
2001US-0283512P.
2001US-0283710P.
2001US-0284234P.
2001US-0285325P.
2001US-0285309P.
2001US-0285309P.
2001US-028509P.
2001US-028509P.
2001US-0286068P.
2001US-0287219.
2001US-0287219.
2001US-0287219.
2001US-029484P.
2001US-029484P.
2001US-029484P.
2001US-029484P.
2001US-029484P.
2001US-029484P.
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2001US-029484P.
2001US-029484P.
2001US-029484P.
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RESULT 11
ADR19663
ID ADR19
XX ADR19
XX O7-OC
DT 07-OC
XX drug
CW drug
KW drug
KW hepat
KW hepat
KW hepat
KW heman
XX human
XX Homo
XX Homo
XX WO200
XX WO200
XX WO200
PD 04-AF
XX 29-SE
PR 06-OC
PR 20-OC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human polypeptides, termed NOVX, and the polymucleotides encoding them. The polypeptides and polymucleotides are useful for diagnosing disease, and screening for potential therapeutic agents. The sequences are useful for treating metabolic disorders, cardiomyopathy, diabetes, hypertension, congenital heart defects, aortic stenosis, atrial septal defect (ASD), atrioventricular canal defect, ductus arteriosus, pulmonary stenosis, subsortic stenosis, ventricular septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma, atherosclerosis, obesity, infectious disease, amorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's disease, immune disorders, haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease and cancer. Sequences ABU54542-ABU54647 represent human NOVX polypeptides
29-SEP-2000;
06-OCT-2000;
20-OCT-2000;
                                                                                                                                                                                                                                                                   drug metabolising antiinflammatory;
                                                                                                                                                                                                                                  drug metabolising enzyme; DME; cytostatic; immunosuppressive; antiinflammatory; endocrine; ophthalmological; gastrointestinal; hepatotropic; cancer; cell proliferative disorder; autoimmune disorder; inflammatory disorder; endocrine disorder; eye disorder;
                                                                   28-SEP-2001;
                                                                                                                                    WO200226988-A2
                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                      inflammatory disorder; endocrine disorder; gastrointestinal disorder; liver disorder;
                                                                                                                                                                                                                                                                                                                                                            07-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                             ADR19663 standard; protein; 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIPYLEAHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTTWDQHAPGNWAFKDQVAALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REATSYPNICLQNSEWLLLDQHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  581 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLLSQKAFKAIPSIIGVNNHECGFLLPM 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIPYLEAHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALS
                                                                                                                                                                                                                                                                                                                       metabolising enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                            (first entry)
2000US-0236947P.
2000US-0238864P.
2000US-0242323P.
                                                                   2001WO-US030662
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Pred. No. 9.9e-312;
                                                                                                                                                                                                                                                                                                                          (DME) -2
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                                                                                                                                                                                                                                                                                                                         protein sequence
                                                                                                                                                                                                                    eye disorder;
metabolic disorder; enzyme;
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RESULT 12 ADC55524

8XU

ADC55524 ADC55524;

standard; protein;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to novel drug metabolising enzymes (DME) and the nucleotide sequences which encode them. The invention may be useful for the development of compounds with a cytostatic, immunosuppressive, antiinflammatory, endocrine, ophthalmological, gastrointestinal or hepatotropic activity acting as an agonist or antagonist of drug metabolising enzyme activity. The invention may be used in the diagnosis and treatment of disorders associated with decreased or increased expression or activity of drug metabolising enzymes. Such disorders include cancer, cell proliferative disorders, autoimmune/inflammatory, endocrine, eye, gastrointestinal (including liver disorders) and metabolic disorders. The present sequence is that of a human drug metabolising enzyme (DME) of the invention. Note: This sequence did not form part of the printed specification but was obtained in electronic form part of the printed specification but was obtained in electronic format from EPO.
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Best Local
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Lal P,
Ting HZ,
Th RT,
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16-NOV-2000;
22-NOV-2000;
30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 2; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human drug metabolizing enzymes, useful in the diagnosis and treatment disorders associated with aberrant (DME) activity, e.g., cancer and
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DB; ADR19681.
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                                                                                                                                                                                                                                                                                         211
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392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 GPSAEGPQRNTRLGWIQGKQVTVLGSSPVPVNVFLGVPFAAPPLGSLRFTNPQPASPWDNL
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t VS, Gandhi AR,
Lee EA, Lu DAM,
IZ, Sanjanwala MS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REATSYPNICLQNSEWILLIDQHMIKVHYPKFGVSEDCLYINIYAPAHADTGSKLPVIVWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAPPLGSLRFTNPQPASPWDNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     618
                              DLLSQKAFKAI PSI I GVNNHECGFLLPM
                                                                                                                 YEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEPL
                                                                                                                                                   YEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEPL
                                                                                                                                                                                                                               WVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIPYLEAHD
                                                                                                                                                                                                                                                                       WVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIPYLEAHD
                                                                                                                                                                                                                                                                                                                                                                                           PGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REATSYPHICLQNSEWLLLDQHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVWF
DLLSQKAFKAIPSIIGVNNHECGFLLPM
                                                                                                                                                                                                                                                                                                                                                   PGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALS
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; 2000US-0249519P.
; 2000US-0252834P.
; 2000US-0250567P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.5%; Score 328; DB 5; Lilarity 100.0%; Pred. No. 1.1e-311; Conservative 0; Mismatches 0;
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Griffin JA, Hafalia AJA, Ison CH, Kt
Nguyen DB, Arvizu C, Policky JL, Ra
Tang YT, Tribouley CM, Narinder WK;
u Y, Yang J, Yao MG, Yue H;
                                                       358
   419
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ABF69056
ID ABF69056
XX ABF69056
AC ABF69
XX 20-JA
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XX Human
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KW Human
KW Cell-
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Best Local S
Matches 195
 Human; genome mapping; gene therapy; food supplement; virus; fungu cell-proliferative disorder; neurodegenerative disease; bacterial; Parkinson's disease; Alzheimer's disease; autoimmune disease;
                                                   Human polypeptide
                                                                                                 ABP69056;
                                                                                                                     ABP69056 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a polypeptide-human carboxylatase-24.64, the polynucleotide for coding it, the process for preparing the polypeptide by DNA recombination, the application of the polypeptide in treating diseases such as primary hypertension, digestive ulcer, nephrotic, bronchial asthma, tremor, etc, the antagon of the polypeptide and its medical action, and the application of the polynucleotide are new. The present sequence represents human carboxylatase 24.64.
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptide-human carboxylatase-24.64 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Мао У,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-APR-2001; 2001CN-00112736.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human carboxylatase-24.64; primary hypertension; digestive ulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BIOW-)
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                                                                                                                                                                                                                                                                                             418
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DB; ADC55523.
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                                                                                                                                                                                         KEPRVDFWTSTIPLI 552
                                                                                                                                                                                                                                                                FVVPALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDI
                                                                                                                                                                                                                                                                             FVVPALITARYHRDAGAPVYFYBERHRPQCFEDTKDAFVKADHADBVRFVFQGAFLKGDI
                                                                                                                                                                                                                                                                                                            MKEAPETLSGSNKSLALHLIQNILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVF
                                                                                                                                                                                                                                                                                                                         MKEAPEILSGSNKSLALHLIQNILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVF
                                                                                                                                                                             KEPRVDFWTSTIPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 2; 31pp;
                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                       (first entry)
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                                                  SEQ ID NO
                                                                                                                     protein;
                                                                                                                                                                                                                                                                                                                                                      33.6%; bu
100.0%; Pr
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                                                  1103
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Pred. No. 6.8e-182;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chinese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polynucleotide
                                                                                                                                                                                                                                                                                                                                                                             Length 224;
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RESULT 14
AAO05817
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В
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                                                                                                                                                                                                                                                                                                                     CC nucleotide sequence selected from any of 948 sequences (ABZ11119 at CREENING of their mature protein coding portion, active domain coding CC protein or complementary sequences. The polynucleotides are useful for CC identifying expressed genes or for physical mapping of human genome. The cenceded polypeptides (ABP68902-ABP69849) are useful as molecular weight commarkers, as a food supplement, for generating antibodies, in medical commarkers, as a food supplement, for generating antibodies, in medical commanders, as a food supplement, for generating antibodies, in medical complements (CC proliferative disorders (cancer), neurodegenerative diseases (Barkinson's CC proliferative disorders (cancer), neurodegenerative diseases (Barkinson's CC proliferative disorders, myeloid or lymphoid disorders, CC diabetes, lupus) generic disorders, myeloid or lymphoid disorders, cc platelet or coagulation disorders, myeloid or lymphoid disorders, liver CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic), CC arthritis, etc. Note; The sequence data for this patent did not form part CC of the printed specification, but was obtained in electronic format CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated polynucleotide (I) comprising nucleotide sequence selected from any of 948 sequences (ABZ11119-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or coagulation disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAR-2001; 2001US-00799451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAR-2002; 2002WO-US005095.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           multiple sclerosis; diabetes; genetic disorder; wound, burn; infect
arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
haemostatic; vulnerary; fungicide; antibacterial; virucide; protozo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiarthritic.
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210
                                  187 GFFT 190
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DB; ABZ11273.
                                                                                                                                              90
                                                                                                                                                                              67
                                                                                                                                                                                                                                  Similarity
                                                             CLYLNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIF
                                                                                  CLYLNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Zhou P, G
Yang Y, Ma
T, Wang J,
                                                                                                                                    PFAAPPLGSLRFTNPOPASPWDNLREATSYPNLCLONSEWLLLDQHMLKVHYPKFGVSED
                                                                                                                                                         PFAAPPLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHMLKVHYPKFGVSED 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYSEQ INC
                                                                                                                                                                                                                                                                                          266
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                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                       21.3%; 5cc
100.0%; Pr
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Ma Y, Yamazaki V, Chen
, Wang D, Drmanac RT;
                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                Score 124;
Pred. No.
                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                              2.7e-112;
                                                                                                                                                                                                                                                  DB 5;
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R, Wang
                                                                                                                                                                                                                                              Length 266;
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                                                                                                                                                                                                             Indels
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, Ghosh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Z
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ren
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                                                                                                                                      149
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AAO05817,

AAO05817 standard;

protein;

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RESULT 15
AAE20909
ID AAE20
XX
AC AAE20
XX
AC AAE20
XX
DT 01-JU
XX
XX
DE Humar
XX
KW Humar
KW Ostec
KW detcx
XX
XX
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activiny, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cytokine; cell proliferation; cell differentiation; gene the vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-NOV-2001
                                                   Human; carboxylesterase-like enzyme; organophosphorus intoxication;
osteopathic; gene therapy; osteoporosis; antisense therapy; cytostatic;
                                                                                                                                                                                                                 AAE20909 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAI85748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200164835-A2
                                osteopathic; gene therapy; osteoporosis; antisense therapy; cytostati
detoxifying agent; Paget's disease; bone implant degradation; cancer;
                                                                                                          Human carboxylesterase-like enzyme protein #1.
                                                                                                                                               01-JUL-2002
                                                                                                                                                                                   AAE20909
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-2001; 2001WO-US004927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treating e.g. leukemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                   449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide SEQ ID NO 19709
                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                     55;
                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acids and polypeptides, useful for preventing ting e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                 EDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWATFAR 74
                                                                                                                                                                                                                                                                                                                                                 EDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKWMKYWATFAR 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NO 19709; 1399pp + Sequence Listing; English
                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                     9.5%;
                                                                                                                                                                                                                       306
                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                    Score 55; DB Pred. No. 4.7 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell differentiation; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Le
4.7e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 124;
                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosing
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ABG66757

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AC ABG6

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease, such as organophosphorus intoxication, cancer and osteoporosis. CC Compounds that increase the ability of human carboxylesterase-like enzyme to bind to organophosphorus compounds are useful as detoxifying agents. CC Carboxylesterase-like enzyme agonists and antagonists are useful for creating osteoporosis, Paget's disease and degradation of bone implants. Carboxylesterase-like enzyme is useful in cc diagnostic assays for detecting diseases and abnormalities or cc susceptibility to diseases or abnormalities related to the presence of mutations in the nucleic acid sequences which encode the enzyme. The cc coding sequence of carboxylesterase-like enzyme polynucleotide is useful in gene therapy and for generating antisense oligonucleotides or cribozymes which specifically bind to mRNA transcribed from carboxylesterase-like enzyme gene expression. The useful for modulating carboxylesterase-like enzyme gene expression. The gresent sequence is human carboxylesterase-like enzyme gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                       Human; inflammatory condition; shock; sepsis; immune response; cancer; wound healing; central nervous system disease; haematopoiesis; peripheral nervous system disease; amyotrophic lateral sclerosis; tendon; myeloid cell disorder; physhoid cell disorder; bone; cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis; bone degenerative disorder; periodontal disease; reperfusion injury; lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carboxylesterase-like enzyme polypeptide. Carboxylesterase-like enzyme useful for treating a carboxylesterase-like enzyme dysfunction related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide. Carboxylesterase-like enzyme and its DNA are usefu screening for agents which decrease or modulate the activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; Fig 5; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human carboxylesterase-like enzyme polypeptide, regulators of which are useful for preventing and treating organophosphorus intoxication,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAD33344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200206454-A2
                                                                                                                                                                                                                                                                                       Human novel polypeptide #92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG66757 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer and osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FARB ) BAYER AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUL-2000; 2000US-0218564P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUL-2001; 2001WO-EP007919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JAN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ä
                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 relates to a purified human carboxylesterase-like enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1e-43;
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allergic condition; thrombolysis; thrombosis;

coagulation disorder;

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RESULT 17
AAM16665
ID AAM16
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AC AAM16
XZ
DT 12-OC
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DE Pepti
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KW Probe
KW cervi
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                                                                                                                                                                                                                                                                                                                                                   polypeptides. The polynucleotides and polypeptides are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's CC disease, ischaemia-reperfusion injury, shock, sepsis, immune responses and cancer and for promoting wound healing. The sequences are used to induce the proliferation of neural cells and regeneration of nerve and control tissue, and are useful for the treatment of central and peripheral controls. The sequences are involved in chemotactic or chemokinetic extivity, regulation of haematopoises, treatment of myeloid or lymphoid contivity, regulation of haematopoises, treatment of myeloid or lymphoid cregeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, tissue repair, healing of burns, inclisions, ulcers, treatment of osteoporosis, osteoarthritis, bone degenerative disorders and periodontal conferences of the invention are also useful for gut conditions, autoimmune disorders immune deficiency (SCID), bacterial or fungal conditions such as atthma, thrombolysis or thrombosis and conditions such as atthma, thrombolysis or thrombosis conditions such as atthma, thrombolysis or thrombosis conditions such as atthma, thrombolysis or thrombosis conditions of the invention
                                                                                                                                                                                                                                                                              Query Match
Best Local (
                                                                                                                                                                                                                                                                Matches
      Probe; human; microarray; gene expression; cervical epithelial cell;
 cervical cancer.
                                           Peptide #3099
                                                                      12-OCT-2001
                                                                                                   AAM16665;
                                                                                                                             AAM16665 standard;
                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang YT, Goo
Yamazaki V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Page 672; 672pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorders, cancer and promoting wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acids and polypeptides for diagnosis, treatment inflammatory, autoimmune, nervous system, myeloid or lymphoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-NOV-2000; 2000US-00728952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-NOV-2001; 2001WO-US047004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fungal infection
                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                               179 VQYRLGIEGFFTTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIF 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002-508509/54.
                                                                                                                                                                                                                                                                                                                                                 polypeptides
                                                                                                                                                                                                                                                              51;
                                                                                                                                                                                                6 VQYRLGIFGFFTTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDESSVTIF 56
                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYSEQ INC.
                                                                                                                                                                                                                                                                                                                      84 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goodrich RW,
V, Ujwal ML,
                                                                                                                                                                                                                                                             Conservative
                                                                   (first entry
                                 encoded by probe for measuring cervical gene expression
                                                                                                                             protein;
                                                                                                                                                                                                                                                     8.8%; Suc
100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                 invention
                                                                                                                               49
                                                                                                                                                                                                                                                                         Score 51;
Pred. No.
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Ω
                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhou P,
RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polynucleotides and associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             healing.
                                                                                                                                                                                                                                                                     DB 5; Le
2.7e-41;
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                                                                                                                                                                                                                                                                                      Length 84;
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                                                                                                                                                                                                                                                          Indels
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cell
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ABB35649
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                                                                                                                                                                                                                                                                                                                RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
                                                       30-JAN-2001;
                                                                                     09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                               WO200157277-A2
                                                                                                                                          Homo sapiens.
                                                                                                                                                                 Human; foetal liver; gene expression; single exon nucleic acid
                                                                                                                                                                                          Peptide #3155 encoded by human foetal liver single exon probe
                                                                                                                                                                                                                              04-FEB-2002
                                                                                                                                                                                                                                                          ABB35649;
                                                                                                                                                                                                                                                                                  ABB35649 standard; peptide; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; SEQ ID NO 21491; 487pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US000670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                      432 AGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                     AGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMF
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                                                        2001WO-US000669
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                         8.4%; Score 49; DB
100.0%; Pred. No. 1.5
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 49;
1.5e-39;
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RESULT 19
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Best Local Similarity
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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21-SEP-2000; 2
27-SEP-2000; 2
04-OCT-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
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                                                                                                                                                           04-FEB-2000;
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                                                                                                                                                                                                       09-AUG-2001.
                                                                                                                                                                                                                                                                     genetic disorder
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                              WPI; 2001-488897/53.
                                                                                                                                                                                                                           WO200157272-A2
                                                                                                                                                                                                                                                                                                     Peptide #3186 encoded by probe
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                                                                                                                                                                                                                                                sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome-derived single exon nucleic acid probes useful for
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                                                                                                                                                                                                                                                                               microarray;
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                                                                       MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                                    standard; protein; 49
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2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-0236359P.
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; 2000US-0234687P.
; 2000US-0236359P.
; 2000GB-00024263.
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                                                                                                                                                            2000US-0180312P
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                                                                                             2000GB-00024263
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                                                 DK,
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                                                                                                                                                                                                                                                                                human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.4%;
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                                                  Chen
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                                                  Rank
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                                                                                                                                                                                                                                                                                antenatal
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Human genome-derived single exon nucleic gene expression in human placenta.

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for measuring

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RESULT 20
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Best Local S
Matches 49
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26-MAY-2000;
30-JUN-2000;
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21-SEP-2000;
27-SEP-2000;
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              The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of the microarray of t
                                                                                                                                                                                                                                                                      Claim 27; SEQ ID
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for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide #3133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human genetic disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-)
                                                                                                                                                                                                                                                                                                              spatially-addressable set of single exon nucleic acid probes, measuring gene expression in sample derived from human breast, prises number of single exon nucleic acid probes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hanzel DK,
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; 2000US-0207456P.
; 2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
; 2000US-0236359P.
; 2000GB-00024263.
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                                                                                                                                                                                                                                                                      NO 13450; 327pp + Sequence Listing;
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far greater diversity of probes
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank
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                                                                                                                                                                                                                                                                      English
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RESULT 21
ABB21078
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  ABA21:35-ABA41305). The present sequence is a protein encoded by one succession in a sample derived from human heart (se probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. It is measuring gene expression, the probes are useful for predicting, measuring sene expression, the probes are useful for predicting, human heart and vascular system e.g. cardiovascular diseases of the hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fifty. Wipo.int/pub/published_pct_sequences
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26-MAY-2000;
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Pred. No.
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                                                                                                                                                                                                                            1.5e-39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probes useful for analyzing
                                                                                                                                                                                                                                                 Length 49;
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                                                                                                                                                                                                                                                                                                                                                           sequence is a
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bone marrow
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AAM56465

standard;

protein;

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RESULT 24
ABG50502
ID ABG50
XX
AC ABG50
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AC ABG50
XX
Unit 25-FE
DT 25-FE
DT 25-FE
DT Humar
XX
Humar
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Homo
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PN WO200
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PD 09-AL
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03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                 probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-483446/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human brain expressed single exon probe encoded protein SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-NOV-2001 (first entry)
                                                                         Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
                                                                                                             Human liver peptide,
                                                                                                                                                                                                                                                                                                                                                Sequence 49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; SEQ ID NO 28570; 650pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US000667
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  09-AUG-2001.
                         WO200157273-A2
                                                Homo sapiens.
                                                                                                                                     25-FEB-2003
                                                                                                                                                                                   ABG50502 standard;
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                                                                                                                                                                                                                                                                                                Similarity 49; Conserv
                                                                                                                                                                                                                                                 Hanzel
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; 2000US-00632366.
; 2000US-0234687P.
; 2000US-0236359P.
; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                 Conservative
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2000US-0207456P.
                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                         invention
                                                                                                                                                                                    peptide;
                                                                                                                                                                                                                                                                                                            8.4%;
                                                                                                             SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                 provides a number of single exon nucleic
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RESULT 25
AAM04381
ID AAM04
XX AAM04
XX O9-OC
XX Probe
KW infla
XX Homo
XX Homo
XX O9-AL
XX O4-FE
PR 20-JH
PR 30-JH
PR 30-JH
PR 30-JH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholasterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                           AAM04381 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
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                                                                        29-JAN-2001;
                                                                                                      09-AUG-2001.
                                                                                                                                  WO200157270-A2
                                                                                                                                                                                        Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma
                                                                                                                                                                                                                                      Peptide #3063 encoded by probe for measuring breast gene expression
                                                                                                                                                                                                                                                                   09-OCT-2001
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21-SEP-2000;
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                                                                                                                                                             sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity 100.
49; Conservative
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; 2000US-0180312P.
; 2000US-0207456P.
; 2000US-00608408.
; 2000US-00632366.
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2000US-0234687P.
2000US-0236359P.
2000US-0024263.
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2000US-00608408.
                                                                                                                                                                                                                                                                 (first entry)
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Pred. No.
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Best Local S
Matches 49
26-MAY-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-006008408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
                                                                                                                                                                                                                 Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                     30-JAN-2001; 2001WO-US000665.
                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                      Human peptide encoded by genome-derived single exon probe SEQ ID 28088
                                                                                                                          15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                               ABG38423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG38423 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (see AA100010-AA110067). The present sequence is a peptide encoded by one a human breast sample, where the probe hybridises at high stringency to a predicting, diagnosing, yrading, straying human gene expression in nucleic acid expressed in the human breast. The probes are useful for diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, particularly those diseases with polygenic inflammatory diseases of the breast fibrovystic changes, proliferative breast disease and non-carcinoma tumours. Note: The sequence data for obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel single exon nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to novel single exon nucleic see AAI00010-AAI10067). The present sequence is a pentide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            432 AGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMF 480
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ilarity 100.0%;
Conservative (
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2000US-0236359P.
2000GB-00024263.
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%; Pred. No. 1.5
0; Mismatches
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. 1.5e-39;
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RESULT 27 AAE20912 ID AAE20

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432 AGAPVYFYEFRHRPQCFEDTKPAPVKADHADEVRFVPGGAFLKGDIVMF

Indels

0

Gaps

0

480 49

AGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMF

Matches

49;

BXBXBX

AAE20912; AAE20912

standard;

peptide; 41

B

01-JUL-2002 (first entry)

Carboxylesterase type-B serine peptide

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CC nucleic acid probes for measuring gene expression in a sample derived CC from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their CC complements or the 12387 open reading frames derived from the 12614 CC; the novel set of probes which hybridise at high stringency to a nucleic concluded are a microarray comprising the novel set of probes (CC acid expressed in the human lung, measuring gene expression in a sample CC collection of detectably abbled nucleic acids derived from human lung (comprising (a) contacting the array with a CC array; identifying exons in a eukaryotic genome, comprising (a) contacting the array with a cC algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably cC having a fragment identical to the predicted exon, the probe is included comprising (a) identifying exons from genomic sequence by the method cc above and (b) measuring the expression of each of the exons in several cc appression of the exons in the tissues and/or cell types using hybridisation to a single exon cc ancer, chronic obstructive pulmonary disease (COPD), interestinal lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interestitial lung tuberous sclerosis, Gaucher's disease, Niemann-pick disease, Hermansky-pudlak syndrome, sarcoidosis, pulmonary haemaniderosis, pulmonary
                               Query Match
Best Local :
                                                                                                              Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                          Sequence 49 AA;
                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a spatially-addressable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-2000; 2000US-0236359P. 04-OCT-2000; 2000GB-00024263.
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                           Similarity
8.4%; So ilarity 100.0%; I Conservative 0;
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                    DB 5; L
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RESULT 28
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ID ADF50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutations in the nucleic acid sequences which encode the enzyme. The coding sequence of carboxylesterase-like enzyme polynucleotide is useful in gene therapy and for generating antisense oligonucleotides or ribozymes which specifically bind to mRNA transcribed from carboxylesterase-like enzyme DNA. These antisense oligonucleotides are useful for modulating carboxylesterase-like enzyme gene expression. The present sequence is carboxylesterase type-B serine peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease, such as organophosphorus intoxication, cancer and osteoporosis. Compounds that increase the ability of human carboxylesterase-like enzyme to bind to organophosphorus compounds are useful as detoxifying agents. Carboxylesterase-like enzyme agonists and antagonists are useful for treating osteoporosis, Paget's disease and degradation of bone implants, particularly dental implants. Carboxylesterase-like enzyme is useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases or abnormalities related to the presence of susceptibility to diseases or abnormalities related to the presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide. Carboxylesterase-like enzyme and its DNA are useful for screening for agents which decrease or modulate the activity of carboxylesterase-like enzyme polypeptide. Carboxylesterase-like enzyme is useful for treating a carboxylesterase-like enzyme dysfunction related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human carboxylesterase-like enzyme polypeptide, regulators of which are useful for preventing and treating organophosphorus intoxication, cancer and osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carboxylesterase-like enzyme; organophosphorus intoxication; enzyme; osteopathic; gene therapy; osteopathic; entisense therapy; cytostatic; detoxifying agent; Paget's disease; bone implant degradation; cancer; dental implant; gene expression; carboxylesterase type-B serine.
                                                                          Cat cauxin protein SEQ ID NO:2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 12; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JUL-2000; 2000US-0218564P
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  Felis catus
                                       cat; cauxin;
                                                                                                                     12-FEB-2004
                                                                                                                                                             ADF50145;
                                                                                                                                                                                                ADF50145 standard; protein; 542 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 41 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a purified human carboxylesterase-like enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-195808/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JUL-2001; 2001WO-EP007919
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                                                                                                                                                                                                                                                                                                                                                                            6.0%; So larity 100.0%; I Conservative 0;
                                     cat kidney disease marker; kidney disease
                                                                                                                   (first entry
                                                                                                                                                                                                                                                                                                                                                                              Score 35; DB 5; L; Pred. No. 6.4e-26; 0; Mismatches 0;
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RESULT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease. (I) enables detection or cat kioney disease samply who correctly. (I) provides an early marker for the disease, and replaces complicated diagnostic methods such as X-ray imaging, ultrasonic imaging,
N-PSDB; ADF50146
                                                                                                                                                                                                                                            cat; cauxin; cat kidney disease marker; kidney disease
                                                                                                                                                                                                                                                                          Cat cauxin protein SEQ ID NO:4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        blood testing.
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                WPI; 2004-002277/01.
                                                                               04-MAR-2002; 2002JP-00057908.
                                                                                                               04-MAR-2002; 2002JP-00057908
                                                                                                                                               09-SEP-2003
                                                                                                                                                                             JP2003250575-A.
                                                                                                                                                                                                             Felis catus
                                                                                                                                                                                                                                                                                                             12-FEB-2004
                                                                                                                                                                                                                                                                                                                                             ADF50147;
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                                                  (TOHO-) TOHOKU TECHNOARCH KK
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31; Conserv
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100.0%;
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The present sequence represents a cat cauxin protein (I) or its salt, which is cat kidney disease marker. Also described: (I) a partial peptide (II) of (I); (2) a nucleic acid (III) encoding (I) or (II); (3) a vector (IV) comprising (III); (4) a transformed host (V) comprising (III) or (IV) comprising (III) or (IV) y (5) producing (I) or (II) by culturing (V); (6) a antibody (VI) or (IV); (5) producing (I) or (II) by culturing (V); (6) a antibody (VI) or (IV); (7) disease which involves measuring (I) quantitatively, and where reduction of amount of (I) indicates presence of the disease; (8) a cat kidney (C) disease diagnostic agent comprising (I) labeling agent, a reagent which compares the biological activity of urinary (I) or (VI); and (9) a cauxin of election kit which measures cauxin in a test sample. (I) is useful as a couxin of the disease in the biological activity of useful for diagnosing cat kidney disease election of cat kidney disease simply and correctly. (I) provides an early marker for the disease, and replaces complicated diagnostic methods such as X-ray imaging, ultrasonic imaging, compared the string of the disease.
                                                                                                                                                                                                                Sequence 542 AA;
                                                                                                                                                                                                                                                                 blood testing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 4; 33pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel cauxin protein or its salt, useful as a cat kidney disease marker, and for diagnosing cat kidney disease.
465 RPVFGGAFLKGDIVMFEGATEBEKLLSRKMM 495
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                                                                                                  Gaps
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Ś Search completed: June 16, 2005, 21:01:29 Job time : 171 secs 밁 Query Match 5.3%; Score 31; DB 8; Length 542; Best Local Similarity 100.0%; Pred. No. 5.9e-21; Matches 31; Conservative 0; Mismatches 0; Indels

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: June 16, 2005, 20:46:43 ; Search time 42 Seconds (without alignments) 1330.999 Million cell updates/sec

Title:
Perfect score:
Sequence: US-10-674-636-2
581
1 MPQGLTSSASQWCFFLILQP......PLSSLTFLSLLQPFFFFFCAP 581

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

PIR\_79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. No matches found Query Score Match Length DB ID Description

Search completed: June 16, 2005, 21:02:15 Job time : 42 secs

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FLJ31547 protein.
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TISSUE=PCR rescued clones;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
Strausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                    NCBI_TaxID=9606;
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SEQUENCE
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InterPro; IPR002018; CarbesteraseB.
InterPro; IPR0020379; Ser estrs.
Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE_B_1;
PROSITE; PS00941; CARBOXYLESTERASE_B_2;
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Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
SIMILARITY: Belongs to the type-B carboxylesterase/lipase
EMBL; BC095501; AAH69501:1; -.
HSSP; P12337; 1K4Y.
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"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                            TKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEBKLLSRKWMKYWATFARTGNPNGN
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                                 DLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIPLILSASDMLHSPLSSLTFLS
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RX MEDLING=22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L. Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Sarcha D., Lux, Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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PubMedel4702039, DOI=10.1038/ng1285;
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Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
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Wakamatsu A., Hayyashi K., Sato H., Magai K., Kimura K., Makita H.,
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Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
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Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
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Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y.,
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Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
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Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
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Sudo H., Kanda K., Yakuta Y., Kodaira H., Kondo H., Sugawara M.,
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Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
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Abe K., Kamihara K., Katsuta N., Sato K., Tujimori K.,
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Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
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Anon Y., Takiguchi S., Watanabe M., Hiraka S., Chiba Y., Ishida S.,
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Cho Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
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Kanehori K., Katasuta H., Jakeuchi K., Arita M., Imose N.,
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Avasahino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
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Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
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Yoshikawa Y., Matanabe K., Kumagai A., Takemoto M., Kawakami B.,
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Yamazaki M., Watanabe K., Kumagai A., Takemoto M., Kawakami B.,
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Yamazaki M., Watanabe K., Kumagai A., Takemoto M., Comori Y.,
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Avawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
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Musahima S., Saaki M., Hirai M., Ikema Y., Okamoto S.,
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Nakai T., Nakamura Y., Matanaba M., Kawakami B.,
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Nakai T., Nakamara Y., Matanaba M., Kawahashi Y., Nakagawa K.,
Complete sequencing and characterization of 21,243 full-length human
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CONAS.", Saada M., Matanaterization of 21,243 full-length human
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Matches 400
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InterPro; IPR000379; Ser_estre.
Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE B 1;
PROSITE; PS00941; CARBOXYLESTERASE_B-2;
Hydrolase; Hypothetical protein.
SEQUENCE 525 AA; 58200 MM; 7724878BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP;
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VANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHR
            Similarity
                                                       DLLSQKAFKAIPSIIGVNNHECGFLLPMKEAPEILSGSNKSLALHLIQNILHIPPPQYLHL
                                         DLLSQKAFKAIPSIIGVNNHECGFLLPMKEAPEILSGSNKSLALHLIQNILHIPPQYLHL
                                                                                      YEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEPL
                                                                                                    YEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEPL
                                                                                                                                   WVQKNIEFFGGDÞSSVTIFGESAGAISVSSLILSÞMAKGLFHKAIMESGVAIIÞÝLEAHD
                                                                                                                                                      WVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIFYLEAHD
                                                                                                                                                                             PGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALS
                                                                                                                                                                                              PGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALS
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                                                                                                                                                                                                                                                                       GPSAEGPÓRNTRLGWIÓGKÓVTVLGSPVPVNVFLGVPFAAPPLGSLRFTNPOPASPWDNL
                                                                                                                                                                                                                                                                                    GPSAEGPORNTRIGWIQGKQVTVLGSPVPVNVFLGVPFAAPPLGSLRFTNBQPASPWDNL
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the type-B carboxylesterase/lipase
                                                                                                                                                                                                                                                                                                                                  Score 400;
Pred. No.
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Homo sapiens (Human).

Eukaryotes / Metazoa, Chordata, Crani Mammalia; Eutheria; Primates; Catal
                              TISSUE=Brain;
PubMed=14702039; DOI
PubMed=14702039; DOI
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01-0CT-2002
01-0CT-2003
 PubMed=14702039; DOI=10.1038/ng1285;
Ota T., Suzuki Y., Nishikawa T., Otsuki T.,
Wakamatsu A., Hayashi K., Sato H., Nagai K.,
Sekine M., Obayashi M., Nishi T., Shibahara
                                                                                                                                                                                                                                               Q8NBC8;
                                                                                       SEQUENCE
                                                                                                                 NCBI_TaxID=9606;
                                                                                     FROM
                                                                                                                                                                                                                           Created)
                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
Otsuki T., Sugiyama T.,
I., Nagai K., Kimura K., I
, Shibahara T., Tanaka T
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annotation update)
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"Complete sequencing and characterization of 21,243 full-length human R.) Takanabe M., Sasaki M., Nakagawa K., R., Watanabe M., Kakuchi H., Masuho Y., Yamasahita R., Kondasa Y., Yamasahita R., Kamashi Y., Nakagawa K., R., Ohara O., Isogai T., Sugano S., Yamasahita R., Kamashi K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., Yamasahita R., Kamashi Y., Nakagawa K., R., Nakamura Y., Ohara O., Isogai T., Sugano S., Yamasahita R., Yanasahi M., Yanasahita R., Yanasahita R., Yanasahita R., Yanasahita R., Yanasahita R., Yanasahita R., Yanasahita R., Yanasahita R., Yanas
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SEQUENCE
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PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.

PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.
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EMBL; AK090997; BAC03565.1; -.
HSSP; P12337; 1K4Y.
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                                                                                                                                                                                                                                       LGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAF 472
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                                                                                                       LKGDIVMFEGATEEEKLLSRKMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMS 532
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LGQRLKEPRV 542
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Pred. No. 0;
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Q95KH3;
01-DEC-2001
01-DEC-2001
01-OCT-2003
                      TISSUB=Kidney;

MEDLINE=22459314; PubMed=12401131; DOI=10.1042/BJ20021446;

MISTAIRE-22459314; PubMed=12401131; DOI=10.1042/BJ20021446;

Miyazaki M., Kämile K., Soeta S., Taira H., Yamashita T.;

"Molecular cloning and characterization of a novel carboxylesterase-like protein that is physiologically present at high concentrations:

the urine of domestic cats (Felis catus).";

Biochem. J. 370:101-110(2003).

-i- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family

EMBL; AB045377; BAC22577.1; -.

HSSP; P12337; 1K4Y.

GO; GO:0016787; F:hydrolase activity; TEA.

InterPro; IPR000379; Ser_estrs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8I034
Q8I034;
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Osada N., Hida M., Kusuda J., Tanuma R., Iseki
Suzuki Y., Sugano S., Hashimoto K.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ
-- SIMILARITY: Belongs to the type-B carboxyl
EMBL; AB060873; BAB46884.1;
HSSP; P12337; 1K4Y.
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Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAR-2003 (TYEMBLYE1. 23, Created)
01-WAR-2003 (TYEMBLYE1. 23, Last sequence update)
01-CCT-2003 (TYEMBLYE1. 25, Last annotation update)
Carboxylesterase-like urinary excreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Cauxin;
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Pfam; PF00135; COesterase; 1.
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|GQRLKEPRV 430
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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  COesterase;
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M., Kusuda J., Tanuma R., Iseki K., Hirai M.,
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Pred. No.
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carboxylesterase/lipase
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GENERAL INFORMATION:
APPLICANT: CURTIS, ROTY A. J.
APPLICANT: CURTIS, ROTY A. J.
APPLICANT: CURTIS, SILOS-SAINIAGO, INMACULADA
TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBO)
TITLE OF INVENTION: FAMILY MEMBER AND USES THE
FILE REFERENCE: 10448-122001
CURRENT APPLICATION NUMBER: US/10/023,515
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 60/256,369
PRIOR APPLICATION NUMBER: 60/279,508
PRIOR APPLICATION NUMBER: 60/279,508
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 6
SOCTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 581
TYPE: PRT
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Maximum DB
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Patent No. 6664091
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length: 2000000000
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AND USES THEREOF
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Best Local :
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Similarity 100.0%;
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                RVDFWTSTIPLILSASDMLHSPLSSLTFLSLLQPFFFFFCAP 581
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Perfect score:
Sequence:
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Run on:
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                                                                                                                                                                                                                                                                            Score
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328
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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24: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
25: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
26: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
27: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
28: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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Match
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    GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd
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US-10-674-636-2
US-10-757-262-46
US-10-451-168-91
US-10-094-749-2375
US-10-433-256-10
US-10-451-168-93
US-10-104-047-2219
US-10-114-270-196
US-10-451-168-92
US-10-381-898-2
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                Sequence 2, Appli
Sequence 2, Appli
Sequence 46, Appl
Sequence 91, Appl
Sequence 2375, Ap
Sequence 10, Appl
Sequence 93, Appl
Sequence 2219, Appl
Sequence 196, App
Sequence 197, Appl
Ś
  541 RVDFWTSTIPLILSASDMLHSPLSSLTFLSLLQPFFFFCAP 581
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APPLICANT: CUITIS, ROTY A. J.

APPLICANT: Silos-Santiago, Inmaculada

ITILE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE

ITILE OF INVENTION: FAMILY MEMBER AND USES THEREOF

ITILE OF INVENTION: FAMILY MEMBER AND USES THEREOF

CURRENT FILING DATE: 2003-09-29

PRIOR APPLICATION NUMBER: US/10/674,636

CURRENT FILING DATE: 2001-12-18

PRIOR APPLICATION NUMBER: 60/256,369

PRIOR APPLICATION NUMBER: 60/256,369

PRIOR FILING DATE: 2001-03-28

PRIOR APPLICATION NUMBER: 60/279,508

PRIOR APPLICATION NUMBER: 60/279,508

PRIOR APPLICATION NUMBER: 60/279,508

PRIOR APPLICATION NUMBER: 60/279,508

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US-10-674-636-2
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Best Local
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 100.0%; Score 581; I Similarity 100.0%; Pred. No. 0; 81; Conservative 0; Mismatches
                                                                                                EGATEEEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNNSLGQRLKEP 540
                       RVDFWTSTIPLILSASDMLHSPLSSLTFLSLLQPFFFFFCAP 581
                                                                                                                                                          PALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMF
                                                                                                                                                                                                                                           LILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRT
RVDFWTSTIPLILSASDMLHSPLSSLTFLSLLQPFFFFFCAP
                                                                                                                                                                                   PALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMF
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APPLICANT: Kaitcheti, Venkateswariu
APPLICANT: Kaitcheti, Venkateswariu
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: WETHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: 1405. 636.4421, 5410, 30905, 2448, 4239, 4373, 51164,
TITLE OF INVENTION: 13711, 52872, 14063, 2073, 32544, 4239, 4373, 51164,
TITLE OF INVENTION: 13711, 52872, 14063, 2073, 22345, 2387, 52908, 69112, 14990,
TITLE OF INVENTION: 53010, 16827, 14063, 2073, 3287, 52908, 69112, 14990,
TITLE OF INVENTION: 53010, 16827, 1870, 72245, 2387, 52908, 69112, 14990,
TITLE OF INVENTION: 53010, 16827, 1897, 7619, 18603, 2395, 2554, 8675,
TITLE OF INVENTION: 2158, 8263, 14930, 16816, 17827, 32820, 577, 619, 1423,
TITLE OF INVENTION: 2544, 9626, 13816, 17827, 32820, 577, 619, 1423,
TITLE OF INVENTION: 55053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 581
TYPE: PRT
ORGANISM: Homo sapiens
241 LILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 100.0%; Score 581; Similarity 100.0%; Pred. No. 0;
                                                                                                                                             YRLGIFGFFTTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSS
                                                                                                                                                                                                                                     NVFLGVPFAAPPLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHMLKVHYPK
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                                                                                                      YRLGIFGFFTTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSS
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HAPPLICANT: GLAKO GNOVE LITTLE OF INVESTIONE, NOVEL COMPOUNDS
FILE REFERENCE: GP50039
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR APPLICATION NUMBER: 60/260,482
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR FILING DATE: 2001-01-03
PRIOR FILING DATE: 2001-02-03
PRIOR FILING DATE: 2001-03-04
PRIOR APPLICATION NUMBER: 60/267,97
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/267,988
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PRIOR APPLICATION NUMBER: 60/276,988
PRIOR FILING DATE: 2001-03-19
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-451-168-91
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APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM p.1.c.
APPLICANT: GLAXO GROUP LIMITED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 91, Application US/10451168 Publication No. US20040091969A1
                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                    REATSYPNICLQNSEWILLIDQHWLKVHYPKFGVSEDCLYINIYAPAHADTGSKLPVLVWF 150
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                             REATSYPNLCLQNSEWLLLDQHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVWF
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                                                                                                                                                                                                                                                                                                     DB 15;
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APPLICANT: SEKI, NACHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: MASCHAKA, KENJI
APPLICANT: MASCHAKA, KENJI
APPLICANT: MASCHAKA, KENJI
APPLICANT: MASCHO, YASCHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 90 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATECRIA DATE: 201-09-14
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US-10-094-749-2375
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                                                    ; ORGANISM: Homo sapiens US-10-094-749-2375
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Publication No. US20030219741A1
GENERAL INFORMATION:
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Query Match
                                                                                                           TYPE: PRT
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OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
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YAMAMOTO, JUN-ICHI
ISONO, YUUKO
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IRIE, RYOTARO
TAMECHIKA, ICHIRO
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  Score 400;
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APPLICANT: CHANLA, BRIDGE A.; YANG, JUMBIN APPLICANT: CHANLA, MARINDER K.; MCGYEN, Dan APPLICANT: ISON, CTAIGH.

APPLICANT: ISON, CTAIGH.

TITLE OF INVENTION: DRIG METABOLIZING ENZYME FILL REFERENCE: PI-0313 USN
CURRENT APPLICATION NUMBER: US/10/433,256
CURRENT FILING DATE: 2003-05-30
PRIOR APPLICATION NUMBER: PT/US01/47429
PRIOR APPLICATION NUMBER: US 60/254,308
PRIOR FILING DATE: 2000-12-08
PRIOR PPLICATION NUMBER: US 60/256,189
PRIOR PPLICATION NUMBER: US 60/257,713
PRIOR APPLICATION NUMBER: US 60/267,706
PRIOR APPLICATION NUMBER: US 60/267,706
PRIOR APPLICATION NUMBER: US 60/267,706
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US-10-433-256-10
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APPLICANT: AU-YOUNG, Janice K.; BAUGHN, M.;
APPLICANT: AUZZU, Chandra S.; RING, Huij
APPLICANT: LEE, Ernestine A.; DING, Li
APPLICANT: HAFALIA, April J.A.; TANG, Y.
APPLICANT: YUE, Henry; TRIBOULEY, Catheri,
APPLICANT: LU, Dyung Alia M.; LAL, Proeti
APPLICANT: WARREN, Bridget A.; YANG, Junm
                                                                                                                                                                     SOFTWARE: PERL Program
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application No. US2
                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                 FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No:
                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                 ENGTH: 642
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YUE, Henry; TRIBOULEY, Catherine M.
LU, Dyung Aina M.; LAL, Preeti G.
WARREN, Bridget A.; YANG, Junming
CHAWLA, Narinder K.; NGUYEN, Danniel
GANDHI, Ameena R.; LU, Yan
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HN, Mariah R.
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CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: E07/US01/49232
PRIOR FILING DATE: 2000-12-17
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR FILING DATE: 2000-12-70
PRIOR PPLICATION NUMBER: 60/257,048
PRIOR PPLICATION NUMBER: 60/260,482
PRIOR FILING DATE: 2001-12-20
PRIOR PPLICATION NUMBER: 60/264,922
PRIOR PILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR PILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR PILING DATE: 2001-03-06
PRIOR PILING DATE: 2001-03-19
PRIOR PILING DATE: 2001-03-19
PRIOR PILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR FILING DATE: 2001-04-04
PRIOR FILING DATE: 2002-06-28
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US-10-451-168-93
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Publication No. US20040091969A1
GENERAL INFORMATION:
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Best Local S
Matches 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: GP50039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 GPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAPPLGSLRFTNPQPASPWDNL
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DL 573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REATSYPNICCLONSEWILLLDQHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVWF
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Pred. No. 0;
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PRIOR APPLICATION NUMBER:
PRIOR FILLING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2219
LENCTH: 469
TYPE: PRT
ORGANISM: Homo sapiens
US-10-104-047-2219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-451-168-93
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Best Local Similarity
Matches 340; Conser
                                                                                                                                                                                                          Matches 429;
                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. US20030236392A1e1 full length
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                482
                                                                                                                                                             113 MLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYE 172
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 121
                                233
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                                                                                     DVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGES 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VDFWTSTIPLILSASDMLHSPLSSLTFLSLLQPFFFFFCAP 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFE 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEILSGSNKSLALHLIQNILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVP 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSKELLTLSQKTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPMKEA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRTK 76
                AGAISVSSLILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSE
                                                                                                                                         MLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VDFWTSTIPLILSASDMLHSPLSSLTFLSLLQPFFFFCAP
AGAISVSSLILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSE
                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                           56.6%;
                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                         Score 329; DB 15;
Pred. No. 1.1e-302;
                                                                                                                                                                                                                                             DB 15; Length 469;
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RESULT 9
US-10-114-270-196
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APPLICANT: Rothenberg, Mark E.
TITLE OF INVENTION: No. US200440303110Alel Proteins and
FILE REFERENCE: 21402-322C
CURRENT APPLICATION NUMBER: US/10/114,270
CURRENT FILLING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/281,086
PRIOR APPLICATION NUMBER: 60/281,086
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR FILLING DATE: 2001-04-03
PRIOR FILLING DATE: 2001-04-03
PRIOR FILLING DATE: 2001-04-03
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                                            OR APPLICATION NUMBER: 60/281,863
OR FILING DATE: 2001-04-05
OR APPLICATION NUMBER: 60/281,906
OR FILING DATE: 2001-04-05
OR APPLICATION NUMBER: 60/282,020
OR FILING DATE: 2001-04-06
OR FILING DATE: 2001-04-06
ADDITION TO NUMBER: 60/282,930 APPLICATION NUMBER: 60/282,930 ADDITION TO NUMBER: 2001-04-10
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r: Kekuda, Ramesh
Miller, Charles B.
Malyankar; Uriel M.
Spyrek, Kimberly A.
Patturajan, Meera
Liu, Ziaohong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smithson, Glennda
Burgess, Catherine E.
Gerlach, Valerie
Padigaru, Muralidhara
Shimkets, Richard A.
Gangolli, Esha A.
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Edinger, Shlomit R.
Stone, David J.
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Shenoy, Suresh G.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vladimir Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                             David W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Raymond
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Same

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Sequence 92, Application US/10451168
Publication No. US20040091969A1
GENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM P.1.C.
APPLICANT: SMITHKLINE BEECHAM P.1.C.
APPLICANT: SMITHKLINE BEECHAM P.1.C.
APPLICANT: SMITHKLINE BEECHAM P.1.C.
ITILE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50039
FILE REFERENCE: GP50039
FILE REPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2000-12-17
PRIOR APPLICATION NUMBER: FCT/US01/49232
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR FILING DATE: 2000-12-17
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR APPLICATION NUMBER: 60/260,482
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR APPLICATION NUMBER: 60/264,922
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; LENGTH: 581
; TYDE: PRT
; TYDE: PRT
; ORCANISM: Homo sapiens
US-10-114-270-196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-10-451-168-92
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; PRIOR APPLICATION NUMBER: 60/283,512
; PRIOR ETLING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 470
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Best Local
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hes 328; Conserv
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100.0%; Pred. No. 1.2e-301;
tive 0; Mismatches 0;
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RESULT 11
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Sequence 2, Application US/10381898 Publication No. US20040086887A1
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NUMBER OF SEQ ID NOS: 110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 92
                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 581
TYPE: PRT
ORGANISM: Homo :
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                                                                          DLLSOKAFKAIPSIIGVNNHECGFLLPM
                                                                                           DLLSQKAFKAIPSIIGVNNHECGFLLPM 358
                                                                                                                      YEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEPL
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Pred. No. 1.2e-301;
0; Mismatches 0;
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Sequence 2, Application US/10381898
Publication No. US20040086887A1
GENERAL INFORMATION:
APPLICANT: AZIMZAI, Yalda; BAUGHN, Mariah R.;
APPLICANT: BOROWSKY, Mark L.; DING, Li;
APPLICANT: BOROWSKY, Mark L.; DING, Li;
APPLICANT: BOROWSKY, Mark L.; DING, Caig H.;
APPLICANT: BOROWSKY, Mark L.; DING, Craig H.;
APPLICANT: HAFALIA, April J.A.; ISON, Craig H.;
APPLICANT: HAFALIA, April J.A.; ISON, Craig H.;
APPLICANT: KHAN, Farrah A.; LAL, Preeti G.;
APPLICANT: RANKUMAR, Jayalaxmi; RING, Huijun Z.;
APPLICANT: RANKUMAR, Jayalaxmi; RING, Huijun Z.;
APPLICANT: TANG, Y. Tom; TRIBOULEY, Catherine M.;
APPLICANT: CHAMLA, Narinder K.; WALSH, Roderick T.;
APPLICANT: YANG, Junning; XAO, Monique; YUE, Henry
TAPLICANT: YANG, Junning; XAO, Monique; YUE, Henry
TILE OF INVENTION INVEST: US/10/381,898
CURRENT APPLICATION NUMBER: US 60/236,947
PRIOR APPLICATION NUMBER: US 60/236,947
PRIOR PILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-10-06
PRIOR PILING DATE: 2000-10-06
PRIOR PILING DATE: 2000-10-0
PRIOR PILING DATE: 2000-10-0
PRIOR PILING DATE: 2000-10-0
PRIOR APPLICATION NUMBER: US 60/247,581
PRIOR FILING DATE: 2000-10-0
PRIOR PILING DATE: 2000-11-09
PRIOR FILING DATE: 2000-11-09
PRIOR FILING DATE: 2000-11-09
PRIOR FILING DATE: 2000-11-06
PRIOR FILING DATE: 2000-11-06
PRIOR FILING DATE: 2000-11-06
PRIOR FILING DATE: 2000-11-06
PRIOR FILING DATE: 2000-11-06
PRIOR FILING DATE: 2000-11-09
PRIOR FILING DATE: 2000-11-09
PRIOR FILING DATE: 2000-11-06
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LENGTH: 618
TYPE: PRT
ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 7473645CD1
US-10-381-898-2
            CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
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PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: US 60/250,567
PRIOR FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PERL Program
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 328; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Penn, Sharron G.
APPLICANT: Rank David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wenebeng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: Aeomica-X-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09864761
NUMBER: PCT/US01/00664
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HELLO, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BTATA, SIGNAL = 3.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7
OTHER INFORMATION: SWISSPROT HIT: Q04791, EVALUE 2.00e-09
                                                                                                                             Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 36376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OR FILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/US01/00663

OR APPLICATION NUMBER: PCT/US01/00662

OR APPLICATION NUMBER: PCT/US01/00662

OR FILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/US01/00661

OR APPLICATION NUMBER: PCT/US01/00661

OR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00668
                                  432 AGAPVYFYBFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMF
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                                                                                                         49;
                                                                                                                                Similarity
                                                                                                         Conservative
                                                                                                      8.4%; Score 49;
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tive 0; Mismatc
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RESULT 13
US-10-233-933A-2
US-10-233-933A-2
; Sequence 2, Application US/10233933A

publication No. US20040214171A1
; Publication No. US20040214171A1
; Publication No. US20040214171A1
; Publication No. US2004021471A1
; Publication Numasa
; Publication Numasa
; Pilk Reference: SHIG FP02US006
; CURRENT APPLICATION NUMBER: US/10/233,933A
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: JP2002-057908
; PRIOR APPLICATION NUMBER: JP2002-057908
; PRIOR APPLICATION NUMBER: JP2002-057908
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 542
; TYPE: PRI
; ORGANISM: Felis Catus
US-10-233-933A-2

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Sequence 4, Application US/10233933A
Publication No. US20040214171A1
GENERAL INFORMATION:
APPLICANT: Yamashita, Tetsuro
APPLICANT: Miyazaki, Masao
TITLE OF INVENTION: CAT KIDNEY DISEASE MARKER
FILE REFERENCE: SHIG FP02US006
CURRENT APPLICATION NUMBER: US/10/233,933A
CURRENT FILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: JP2002-057908
PRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 542
TYPE: PRT
ORGANISM: Felis catus
US-10-233-933A-4
Search completed: June 16, 2005, 21:18:08 Job time: 160 secs
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US-10-233-933A-4
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                                                                                                                                               Query Match 5.3%; Score 31; DB 16; Length 542; Best Local Similarity 100.0%; Pred. No. 3.4e-20; Matches 31; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.3%; Score 31; DB 16; Length 542; Best Local Similarity 100.0%; Pred. No. 3.4e-20; Matches 31; Conservative 0; Mismatches 0; Indels
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